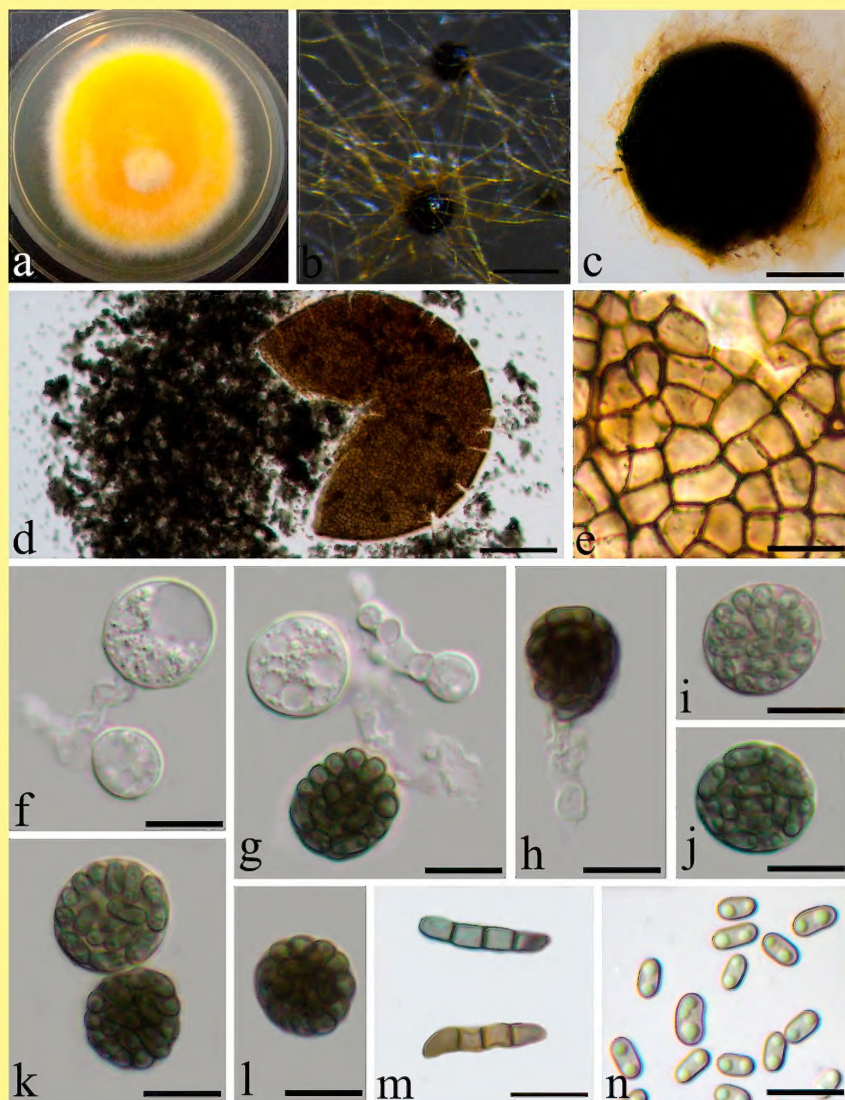


MYCOTAXON

THE INTERNATIONAL JOURNAL OF FUNGAL TAXONOMY & NOMENCLATURE

VOLUME 135 (2)

APRIL–JUNE 2020



Westerdykella aquatica sp. nov.

(Song & al.— FIG. 2, p. 289)

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MYCOTAXON

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	READ: A. NASEER, S. KHANUM, A.R. NIAZI, A.N. KHALID	241
p.241, line 6	FOR: A. NASEER ^{1*} , S. GHANI ² , A.R. NIAZI ² , A.N. KHALID ²	
	READ: A. NASEER ^{1*} , S. KHANUM ² , A.R. NIAZI ² , A.N. KHALID ²	

REVIEWERS — VOLUME ONE HUNDRED THIRTY-FIVE (2)

The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

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2020 MYCOTAXON SUBMISSION PROCEDURE

Prospective MYCOTAXON authors should download the MYCOTAXON 2020 guide, review & submission forms, and MYCOTAXON sample manuscript by clicking the 'file download page' link on our INSTRUCTIONS TO AUTHORS page before preparing their manuscript. This page briefly summarizes our '4-step' submission process.

1—PEER REVIEW: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2020 MYCOTAXON journal or mycota reviewer comment form. Experts return revisions & comments to BOTH the *Editor-in-Chief* <editor@mycotaxon.com> and authors. ALL co-authors MUST correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—NOMENCLATURAL REVIEW: Authors email all **ERROR-FREE** text & illustration files to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname + genus + 'MYCOTAXON'** on the subject line, and (required) attach a completed SUBMISSION FORM. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—FINAL SUBMISSION: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a (i) revised 2020 submission form, all (ii) text files and (iii) jpg images, and (iv) FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—FINAL EDITORIAL REVIEW & PUBLICATION: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

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FROM THE EDITOR-IN-CHIEF

COLLABORATION & THE MULTI-AUTHORED PAPER—Mycological taxonomic research is no longer a simple matter of reaching down, plucking a fungus from its substrate, seeing something REALLY different, checking the microscopical characters, reading the one or two papers ever written on aforesaid fungal family, and then writing a paper. Current fungal taxonomy encompasses a great many disciplines, including (but not limited to) microscopy, ecology, physiology, mating studies, ultrastructure, systematics, DNA extractions, sequence analyses, and evolutionary relationships. Yet we somehow expect students injected into this bewildering maelstrom of disciplines to be able (eventually) to present their research in the form of a published paper.

As only a limited number of geniuses can master all modern disciplines, there are now relatively few solo-authored papers. Most research papers are crafted by an agreeable consortium of individuals, each of whom contributes one or two expert pieces that flesh out the final manuscript. The individual who bears the greatest responsibility (and gets—however little deserved—most of the credit) is the first author. All students must oversee all stages of each manuscript submission to ensure that they master the scientific publication process. The first named author bears the responsibility for ensuring that a manuscript meets all journal requirements and seeing that all facts are coherently written and correct. Generally it is that author who discusses the research with all whose names will stand on the final publication. It is also generally the first author who gathers all contributors together to work out a complication and perfect the final text whenever an error or oversight is detected.

Nonetheless, a multi-authored paper is NOT a work by one author. Journals such as MYCOTAXON expect ALL contributing authors to read and revise numerous drafts thoroughly, to check all drawings, tables, and data, and communicate with the first author throughout the research process and prior to submission. Editors expect to receive papers that have been—by *all* authors—thoroughly proofed and that contain no scientific, grammatical, or visual errors. Only through rigorous oversight by all collaborators, particularly the more experienced and knowledgeable among them, is it possible for a beginning scientist to publish in a well-established international scientific journal.

We heartily urge all of our authors to discuss their research among themselves and with their lab mates. That way lies progress!

DEAR READERS (PLUS PREMATURE THANKS TO THE MYCOTAXON EDITORIAL BOARD)—Your editors are currently swamped with submissions—the expected result of discontinuing required page charges in 2018. For sixteen years, Dr. Pennycook has tirelessly accessioned and examined manuscripts, gradually adding scientific and grammatical oversight to his already heavy nomenclatural duties. In the process, he has nomenclaturally accepted almost 2000 manuscripts, rejected ~100, and is currently reviewing 105 more. In its search for scientifically rigorous and nomenclaturally correct papers produced by dedicated authors and their expert

reviewers, MYCOTAXON still needs Shaun's nomenclatural knowledge because so few mycologists fully understand the rules of the International Code of Nomenclature.

Needless to say, both authors and editors are unhappy with the current lengthy time between manuscript accession and return of the nomenclatural review.

However, it now appears that all too often, author-selected experts do not devote the time needed for rigorous review, so that Dr. Pennycook frequently accessions manuscripts that require much more work. With many problems not detected by a quick scan of accessioned files, frequently only after Shaun has begun a review does he discover that the unsatisfactory files must be returned to authors for more work. Not surprisingly, this further lengthens the time between accession and nomenclatural approval.

Three months ago we decided that Shaun could work through his backlog more quickly by focusing only on nomenclature and by returning all other grammatical and scientific edits to the Editor-in-Chief (me). Unfortunately after encountering far too many scientific errors or inaccurate citations, I now must also double-check GenBank, herbarium records, and – yes – even scale bars for accuracy and consistency.

Fortunately, learning in June that your two volunteer editors needed at least one extra pair of eyes, editorial board member Else Vellinga volunteered to serve as MYCOTAXON's first 'official' PRELIMINARY READER. She offered to glance through still unreviewed manuscripts to determine which authors properly implemented expert suggestions, formatted grammatically correct text files, and presented no scientific contradictions as well as flag those papers needing additional work. Dr. Vellinga surveyed several manuscripts—happily finding one in excellent shape and less happily finding several in need of considerable repair or additional research prior to nomenclatural review.

In our estimation, Else, who delivered thorough reviews forwarded to the authors, has been a rousing success. We now plan to contact other board members to help us determine which other accessions are ready for nomenclatural review, which need additional research, and which should be rejected. Authors able to make any suggested changes and return them before Shaun begins his review will not lose their place in the nomenclatural 'queue.'

We sincerely hope this will help shorten our review turn-around time and give your volunteer editors much needed assistance in their currently overwhelming editorial duties. We both dearly desire returning to a time when all submissions were so well prepared that all we need do is to rubber-stamp "approved" after the first read-through. 'Tis a consummation devoutly to be wished.

MYCOTAXON 135(2) provides 22 papers and announces three mycobiota by 88 authors (from 23 countries) reviewed by 54 experts.

The 2020 April–June MYCOTAXON sets forth ONE new genus (*Ramiphialis* from Brazil) and EIGHT species new to science representing *Acarospora* & *Sarcogyne* from

the US & CANADA; *Armillaria*, *Haematomma*, *Vanderbylia*, and *Westerdykella* from CHINA; *Coprinellus* from PAKISTAN; and *Ramiphialis* from BRAZIL. Authors also offer three new combinations in *Cercosporella*, *Ellismarsporium*, and *Microthecium*.

Range extensions are reported for [ascomycetes] the powdery mildew *Golovinomyces* (CHINA) and truffle *Elaphomyces* (TURKEY); [basidiomycetes] the agarics *Pluteus* (EUROPE) & *Xerula* (ARGENTINA), secotiid *Entoloma* (SLOVAKIA), and rust *Aecidium* (PAKISTAN); [lichens] the leprose *Lepraria* (IRAN), assorted graphidoid & thelotremoid taxa (INDIA), and crustose *Carbonea* & *Rinodina* (POLAND); and [myxomycetes] the slime molds *Badhamia* & *Trichia* (BELARUS).

We also offer phylogenetic explorations of *Acrospeira*, *Armillaria*, *Coprinellus*, *Ellismarsporium*, *Golovinomyces*, *Pluteus*, *Vanderbylia*, and *Westerdykella*; a key to the *Lepraria* species of Iran; reevaluation of three *Calicium* taxa proposed in 1909; and a comprehensive index of fungal names derived from te reo Māori. Finally, we announce three new www.mycotaxon.com mycobiota covering Australian marine fungi, Brazilian corticioids, and a global list of aquatic glomeromycotans.

Best wishes for excellent health and with warm regards,

Lorelei L. Norvell (*Editor-in-Chief*)
8 July 2020

Four new *Lepraria* species for Iran, with a key to all Iranian species

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ABSTRACT—*Lepraria eburnea*, *L. ecorticata*, *L. jackii*, and *L. leuckertiana*, found in deciduous forests in Golestan province, are recorded for the first time from Iran. Descriptions and illustrations of all four species and a key to all *Lepraria* species known from Iran are provided.

KEY WORDS—Hyrcanian forest, leprose lichens, sterile lichens

Introduction

Species of *Lepraria* Ach. (*Stereocaulaceae*, *Lecanoromycetes*) are characterized by thalli completely composed of more or less clusters of soredia resting on a continuous medulla (Lendemer 2013). They lack ascocarps or conidia; therefore with few morphological features available as taxonomic characters, the presence of secondary metabolites plays a significant role in distinguishing species (Leuckert & al. 1995, Saag & al. 2009). DNA analyses by Ekman & Tønsberg (2002) confirmed the taxonomic status of the genus and its species. ITS analysis by Bayerová & al. (2005) showed that species may be distinguished through subtle differences in aliphatic acid content, difficult to trace using the usual TLC methods.

Lepraria is widely distributed with 61 species currently known worldwide (Sipman 2004, Saag & al. 2009, Matwiejuk 2017). In Asia it is known from Armenia, China, India, Mongolia, Pakistan, Singapore, Tajikistan, and Turkey. Eleven species have been reported from Iran: Sohrabi & Orange (2006) and Sohrabi & al. (2010) report *L. lobificans* Nyl. and *L. diffusa* (J.R. Laundon) Kukwa from Golestan and Mazandaran provinces, *L. vouauxii* (Hue) R.C. Harris from East Azerbaijan and Golestan provinces, *L. crassissima* (Hue) Lettau from Mazandaran, and *L. alpina* (B. de Lesd.) Tretiach & Baruffo and *L. nivalis* J.R. Laundon from Zanjan province; Valadbeigi & al. (2009) report *L. isidiata* (Llimona) Llimona & A. Crespo from Ilam; Haji Moniri & Kukwa (2009) report *L. caesia* (B. de Lesd.) J.R. Laundon and *L. rigidula* (B. de Lesd.) Tønsberg from Northern Khorasan; Kukwa & Sohrabi (2008) report *L. impossibilis* Sipman from Mazandaran province; and Dyanat-Nejad & Keramedini (1993) report *L. membranacea* (Dicks.) Vain. from Tehran province.

The Golestan province is particularly promising for lichens due to its extensive Hyrcanian forests dominated by *Parrotia persica* (DC.) C.A. Mey., *Quercus castaneifolia* C.A. Mey., *Acer velutinum* Boiss., *Gleditsia caspia* Desf., *Pyrus boissieriana* Buhse, and *Alnus subcordata* C.A. Mey. (Akhani & al. 2010). Only three *Lepraria* species have previously been identified from Golestan province (Sohrabi & Orange 2006): *L. lobificans*, *L. diffusa*, and *L. vouauxii*. We report new to Iran and describe four additional species from Naharkhoran Forest in Golestan found in wet and shady habitats, often on thick *Quercus* bark and on mosses over bark. We also provide a key to all *Lepraria* species known from Iran, including *L. finkii* (B. de Lesd.) R.C. Harris, which has been confused with *L. lobificans* (Lendemer 2013).

Material & methods

The specimens are deposited in the Herbarium, Research Institute of Forests and Rangelands, Tehran, Iran (TARI) and were compared with herbarium samples in the Herbarium, Botanischer Garten und Botanisches Museum Berlin-Dahlem, Berlin, Germany (B). Morphological and anatomical characters were observed with a Luxeo 4D stereomicroscope and a Zeiss compound microscope. The chemistry was analyzed with thin layer chromatography (TLC) following Orange & al. (2010) and Elix (2014) using solvent systems A (toluene, dioxane, acetic acid), B' (hexane, diethyl ether, formic acid), and C (toluene, acetic acid). For identification, the keys of Saag & al. (2009) and Knudsen & Elix (2007) were also used.

Taxonomy

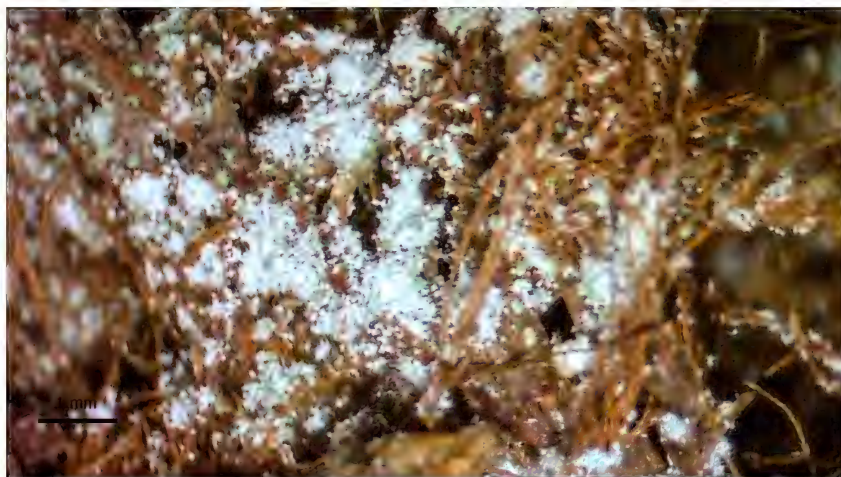


FIG. 1. *Lepraria eburnea* (TARI, Kazemi 9023).

Lepraria eburnea J.R. Laundon, Lichenologist 24: 332. 1992.

FIG. 1

TYPE: British Isles, England, London Borough of Hammersmith and Fulham (V.C. 21, Middlesex), All Saints Fulham churchyard, 51/243759, in slight shade on moss, brick, and mortar on vertical surface of brick wall on east side of churchyard, 30.vi.1987, on calcareous rocks, J.R. Laundon 3185 (BM [n.v.], holotype).

Thallus white-grey to white-green, turning pale pink in the herbarium due to its alectorialic acid content, thick, leprose, placodioid, without wrinkled margin, diffuse, persistent and clearly two-layered, initially forming small patches of thallus that are later incorporated into the margin, without lobes; hyphae unilateral, hyaline, septate; initially with prothallus; hypothallus with variously developed layer of hyphae around and under the granules, thick and white, without rhizohyphae, granules spherical, fuzzy, and ecorticate, with short projecting hyphae, forming multiplex units (consoredia).

CHEMISTRY: thallus K+ yellow, C+ yellow, KC+ pink.

TLC: Alectorialic acid, protocetraric acid.

SPECIMEN EXAMINED: IRAN, GOLESTAN PROVINCE: Gorgan, Alangdareh Forest, around health road, 36.7928°N 54.4504°E, 341 m, 16.11.2017, Kazemi 9023 (TARI).

COMMENTS: Our material agrees with the most detailed descriptions of *L. eburnea* presented by Saag & al. (2009), Kukwa (2006), and Tsurukau & al. (2016).

Lepraria eburnea is similar to *L. nivalis*, in that both species have protocetraric acid and grow on mosses; however, *L. nivalis* differs by its growth on mosses covering calcareous rocks, not bark and its absence of alectorialic acid.

Lepraria eburnea is morphologically similar to *L. finkii* in that both have a thick white medulla; they are separated by chemical differences: *L. finkii* has atranorin, stictic acid, and zeorin as secondary metabolites.

HABITAT: *Lepraria eburnea* grows on sheltered microhabitats in mountainous regions as well as on partially shaded moss, brick, and mortar on vertical brick wall surfaces and on acidic substrates, soil, *Alnus glutinosa*, and *Quercus robur* (Laundon 1992, Kukwa 2006, Lendemer 2013). The specimen reported here was found on mosses on large *Quercus castaneifolia* tree in Hyrcanian forest.

GEOGRAPHICAL DISTRIBUTION: Asia (Armenia, Turkey) (Gasparyan & Sipman 2016, Cobanoglu & Akdemir 2000), Europe, North America (Saag 2009).

Lepraria ecorticata (J.R. Laundon) Kukwa, Mycotaxon 97: 64. 2006

FIG. 2

TYPE: British Isles, England, Devon [vice-c 4], Ilfracombe, Torrs Walks, 21/50 47, on shaded vertical rocks, 1 September 1971, J.R. Laundon 2851 (BM [n.v.], holotype).

Thallus yellowish-green to bluish-grey, leprose; without margin, granules in to irregular mass, without lobes; medulla thin and pale, rarely differentiated, often absent; hyphae aggregate, without septa, pale, covered with granular crystals, soredia abundant, without projecting hyphae, ecorticate, mostly fine to medium, well separated from one another.

CHEMISTRY: K+ pale yellow, C–, KC–, Pd–.

TLC: Atranorin, usnic acid, zeorin.

SPECIMEN EXAMINED: IRAN, GOLESTAN PROVINCE: Gorgan, Naharkhoran road, Delbar mountain, 36.7223°N 54.5490°E, 1049 m, 17.11.2017, Kazemi 8784 (TARI).

COMMENTS: Our specimen agrees with the detailed descriptions of *L. ecorticata* presented by Kukwa (2006), Saag & al. (2009), Laundon (2003), Flakus & Kukwa. (2007).

In Iran *Lepraria ecorticata* is similar chemically with *L. leuckertiana*, as both have usnic acid and zeorin, but *L. ecorticata* is distinguished by having well-separated soredia and lacking a distinct medulla and marginal lobes, while *L. leuckertiana* has irregular and greatly coalescing soredia, a thick medulla, and minute marginal lobes.



FIG. 2. *Lepraria ecorticata* (TARI, Kazemi 8784).

HABITAT: *Lepraria ecorticata* grows on shaded places on acidic rocks, on siliceous and calcareous rocks and walls, and (rarely) on the bark of *Populus*, *Tilia*, and *Fraxinus* (Laundon 2003, Tsurykau & al. 2016). The specimen reported here was found on *Parrotia persica* in montane Hyrcanian forest.

GEOGRAPHICAL DISTRIBUTION: Asia (China), Europe, North America, South America (Kukwa 2006).

Lepraria jackii Tønsberg, Sommerfeltia 14: 200. 1992.

FIG. 3

TYPE: Norway, Nord-Trøndelag, Grong, W of Abrahammyra, 80–100 m, 16.ix.1981, on *Picea abies*, T. Tønsberg 6176 (BG [n.v.], holotype).

Thallus greenish-grey to whitish-green, leprose, without stratified and alternate margin, at first forming separated granules that later accumulate to continuous masses, without marginal zone, without lobes; hyphae unilateral, hyaline; without prothallus; hypothallus absent; without rhizohyphae; granules spherical, well developed, separate, and forming multiplex units; medulla present, white, sparse to continuous; soredia abundant, without projecting hyphae, ecorticate, small, dispersed or forming a thick, continuous layer, sometimes in larger clusters (consoredia).

CHEMISTRY: Thallus K+ yellow, C–, KC–, P+ yellow.

TLC: Atranorin (fatty acids are also reported but were not clearly visible on our plates).

SPECIMEN EXAMINED: IRAN, GOLESTAN PROVINCE: Gorgan, Naharkhoran road, around environmental station, 36.7911°N 54.4665°E, 387 m, Kazemi 9019 (TARI).

COMMENTS: The Iranian material does not show significant differences from the detailed descriptions of *L. jackii* presented by Kukwa (2006), Czarnota & Kukwa (2001), Matwiejuk (2017), Saag & al. (2007), and Tsureykau & al. (2016).

Lepraria jackii can be confused with *L. caesioalba* as both have atranorin and similar reactions with K and P, but *L. caesioalba* can be distinguished morphologically by its obscure sublobes while *L. jackii* completely lacks lobes.

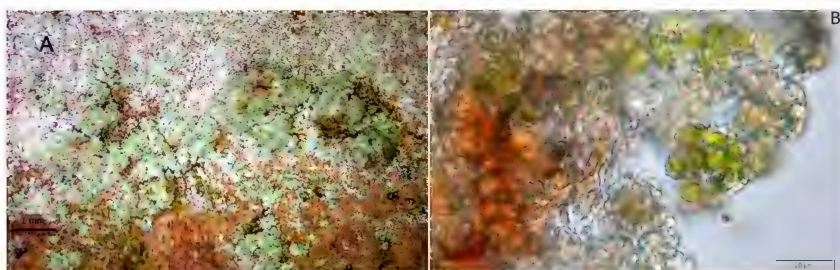


FIG. 3. *Lepraria jackii* (TARI, Kazemi 9019).
a. Thallus; b. Photobiont cells.

HABITAT: *Lepraria jackii* grows on conifers (*Picea abies*) and rarely on sheltered rocks or humus, on mosses and soil, and sometimes on other lichens (Tønsberg 1992, Saag & al. 2007, Lendemer 2013). The specimen reported here was found on *Zelkova carpiniifolia* bark in a Hyrcanian forest.

GEOGRAPHICAL DISTRIBUTION: Asia (Armenia) (Gasparyan & Sipman 2016), Europe, North America, Australia (Saag 2009).

Lepraria leuckertiana (Zedda) L. Saag, Lichenologist 41: 41. 2009.

FIG. 4

TYPE: Italy: Sardinia: Prov. Sassari: Illorai, Monte Artu, 1494647E, 4472420N (Gauss-Boaga), 840 m, on bark and mosses on old *Quercus pubescens* Willd. trees in a mixed wood of *Q. pubescens* and *Q. ilex* L., in open conditions, 9.4.1997, L. Zedda 1800(2) (B [n.v.], holotype; herb Zedda and SS [n.v.], isotypes).

Thallus greenish-white to greenish-grey, leprose, thick and powdery to granular; without margin, often sublobate, hyphae condensed, pale; prothallus absent; medulla white, exposed in some parts, forming a thick layer; soredia abundant, granular, fine to coarse, gathered into consoredia. Soralia ecorticate, with short projecting hyphae, hyphae to 4-5 µm diam., pale and branched, unorganized.

CHEMISTRY: Thallus K-, C-, Pd-, KC-.

TLC: Usnic acid, zeorin; isousnic acid is also reported but was not clearly visible on our plates.

SPECIMEN EXAMINED: IRAN, GOLESTAN PROVINCE: Gorgan, Naharkhoran road, Delbar mountain, 36.7467°N 54.5001°E, 1092 m, 17.11.2017, Kazemi 8784 (TARI).

COMMENTS: Our specimen agrees fully with the detailed descriptions of *L. leuckertiana* presented by Saag & al. 2009, Zedda 2000.

Morphologically *L. leuckertiana* resembles *L. vouauxii* but differs in spot test and chemistry; chemically *L. leuckertiana* resembles *L. ecorticata* and differs by the strongly agglutinating, not well separated soredia.

HABITAT: *Lepraria leuckertiana* grows on old trees (especially on *Quercus*), on palm and olive trees, and on sandy soil and roots (Zedda 2000). The specimen reported here was found on *Quercus castaneifolia* bark in a montane Hyrcanian forest.

GEOGRAPHICAL DISTRIBUTION: Asia (Gasparyan & Sipman 2016, Paukov & al. 2017), Africa, Europe, South America (Saag 2009).



FIG. 4. *Lepraria leuckertiana* (TARI, Kazemi 8784).

Key to the *Lepraria* species in Iran

- 1 Thallus surface granular; soredia coarse, >100 µm in diam.,
sometimes elongate and isidium-like 2
- Thallus surface powdery; soredia mostly <80 µm in diam. 5
- 2 On mineral soil; fumarprotocetraric acid present;
granules indistinct, partly elongate and isidioid *L. isidiata*
- On rock or moss over rock; fumarprotocetraric acid absent;
granules distinct, not isidioid 3

3	Stictic acid present; thallus K+ yellow to orange	<i>L. lobificans</i>
	Stictic acid absent; thallus K- or + pale yellow to pale brown	4
4	Thallus K+ brown, Pd + red, with protocetraric acid	<i>L. nivalis</i>
	Thallus K+ yellow, Pd+ yellow, with psoromic acid and atranorin	<i>L. caesiobalba</i>
5	Alectorialic and protocetraric acids present (staining paper brown in herbarium); medulla thick and distinct	<i>L. eburnea</i>
	Alectorialic acid absent (not staining paper in herbarium)	6
6	Divaricatic acid with nordivaricatic acid and zeorin present, soredia C+ red	<i>L. crassissima</i>
	Divaricatic acid absent	7
7	Stictic acid present; soredia K+ yellow to orange	<i>L. finkii</i>
	Stictic acid absent	8
8	Pannaric acid (or pannaric acid derivatives) as primary substance	9
	Pannaric acid and its derivatives absent or present only in trace to minor amounts; other major compound(s) present	12
9	4-Oxypannaric acid 2-methylester as primary substance	<i>L. diffusa</i>
	4-Oxypannaric acid 2-methylester absent or present in only trace to minor amounts; other major dibenzofurans present	10
10	Thallus with distinct lobes; pannaric acid as primary substance, other minor dibenzofurans also present	<i>L. membranacea</i>
	Thallus indistinctly or not lobed; pannaric acid absent or present only in trace to minor amounts, pannaric acid-6-methylester present	11
11	Thallus with distinct lobes with raised marginal rim; lecanoric acid and pannaric acid-6-methylester present; C+ red	<i>L. impossibilis</i>
	Thallus with indistinct lobes without marginal rim; pannaric acid 6-methylester alone present; C-	<i>L. vouauxii</i>
12	Porphyritic acid present	<i>L. alpina</i>
	Porphyritic acid absent; thallus powdery	13
13	Usnic acid and zeorin present	14
	Usnic acid absent, zeorin absent or present	15
14	Medulla thick and cottony	<i>L. leuckertiana</i>
	Medulla thin or absent	<i>L. ecorticata</i>
15	Soredia small, without projecting hyphae	<i>L. jackii</i>
	Soredia large, with projecting hyphae	<i>L. rigidula</i>

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***Pluteus diana*e and *P. punctatus* resurrected, with first records from eastern and northern Europe**

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ABSTRACT—The type specimens of *Pluteus diana*e and *P. punctatus* from the Czech Republic were studied morphologically and molecularly. New collections identified by nrITS sequence analyses extend the distribution of *P. diana*e to Denmark, European Russia, and the Asian part of Turkey and of *P. punctatus* to Sweden. The application of these names is discussed; both belong in the *P. plautus* complex, and data on European and North American taxa in this complex are summarised and compared with *P. diana*e and *P. punctatus*. *Pluteus aestivus* is considered a nomen dubium.

KEY WORDS—Agaricales, Czechia, Pluteaceae, *Pluteus* sect. *Hispidoderma*, taxonomy

Introduction

Pluteus Fr. (Pluteaceae, Agaricales) is an agaricoid genus forming basidiomata characterized by free lamellae, a pinkish spore print, smooth globose to ellipsoid (rarely oblong) basidiospores, an inverse hymenophoral trama, and the presence of cheilocystidia and (often) pleurocystidia (Singer 1986, Vellinga 1990). Singer (1986) distinguished three sections in the genus:

Pluteus sect. *Pluteus*, *P.* sect. *Hispidoderma* Fayod, and *P.* sect. *Celluloderma* Fayod (the last comprising *P.* subsect. *Eucellulodermini* Singer and *P.* subsect. *Mixtini* Singer). *Pluteus* sect. *Hispidoderma* is characterized by non-metuloid cystidia and a pileipellis arranged as a trichoderm or hymeniderm (Vellinga & Schreurs 1985, Justo & al. 2011a); *P. diana*e Pilát and *P. punctatus* Wichanský belong in this section. Within the section, according to Pilát (1968), Vellinga (1990), and in concordance with our morphological and phylogenetical studies, both species can be broadly ascribed to the species complex around *P. plautus* (Weinm.) Gillet. Although many species have been described in the *P. plautus* complex, there still exists taxonomic uncertainty regarding the identity of many of its species. Vellinga & Schreurs (1985) placed 13 names in synonymy with *P. plautus*, while other authors who maintained a narrower taxonomic concept (e.g., Orton 1986) accepted several species in this group (e.g., *P. dryophiloides* P.D. Orton, *P. punctipes* P.D. Orton, *P. granulatus* Bres., *P. depauperatus* Romagn.). Recent molecular phylogenies challenge the broad taxonomic concept of Vellinga & Schreurs and emphasize the need for reevaluating names in this complex based on a combination of morphological, ecological, and molecular data (Justo & al. 2011b). In this article we take a first step toward clarifying the taxonomy of the *P. plautus* complex by focusing on type studies of *P. diana*e and *P. punctatus*.

*Pluteus diana*e was described by Pilát (1968) and *P. punctatus* by Wichanský (1972) based on collections from Czechia (formerly Czechoslovakia). However, no subsequent collections have been reported and no further information on these species has ever been published. Pilát (1968) described *P. diana*e as macroscopically similar to *P. pellitus* (Pers.) P. Kumm., belonging to *P.* subsect. *Depauperati* Lange, a taxon that almost corresponds to *P.* sect. *Hispidoderma* (Lange 1917, Lange 1936, Vellinga & Schreurs 1985). Wichanský (1972) characterized *P. punctatus* by a greyish-brown pileus with dark brown floccose squamules, a whitish stipe densely covered with brown felted squamules, and a pileipellis consisting of very long cylindrical elements.

Materials & methods

Morphology

Macroscopic descriptions of the collected specimens are based on fresh basidiomata. Colour abbreviations follow Kornerup & Wanscher (1983). Morphological terminology follows Vellinga (1988). Microscopic features were studied by H. Ševčíková (holotypes of *P. diana*e, *P. depauperatus*, *P. hiatus*ulus, *P. inflatus*, *P. puberulus*, *P. punctatus*, and Czech collections of *P. granulatus*, *P. plautus* sensu lato, and *P. semibulbosus* sensu lato) on dried material mounted in Congo red using an Olympus BX-50 light microscope

with magnifications of 400 $\times$ and 1000 $\times$. All Russian collections were studied by E.F. Malysheva using an ammonia Congo red solution under a Zeiss Axio Scope.A1 microscope. Collections studied by A. Justo include material from Denmark, Sweden, and all North American holotypes; microscopic features were studied on dried material mounted in 5% KOH or an ammonia Congo red solution under a Leica DFC2500 microscope. Microscopic descriptions were based on at least 30 measurements each of basidiospores, cheilocystidia, pleurocystidia, and caulocystidia and 25 measurements of basidia. The expression 1/1/30 for basidiospores means 1 collection / 1 basidioma / 30 basidiospores measured in total. Abbreviations: avl = mean of basidiospore length; avw = mean of basidiospore width; avg. = average; Q = quotient of length and width in any one basidiospore; avQ = mean of basidiospore Q-values. Herbarium abbreviations follow Thiers (2018). Authors of fungal names are cited according to the International Plant Names Index website (<http://www.ipni.org>).

Molecular phylogeny

DNA EXTRACTION—The type collections of *P. diana*e and *P. punctatus* were sequenced to establish their position in *P. sect. Hispidoderma*. Only dried herbarium specimens were used for DNA extraction. M. Tomšovský extracted the DNA from both holotypes following the protocol of the Qiagen PowerSoil DNA Isolation Kit to step no. 13 (purification of DNA with C2 and C3 buffers) and then continued with MagNA Pure Compact Nucleic Acid Isolation Kit I performed automatically in MagNA Pure Compact Instrument; M. Sochor (Crop Research Institute, Olomouc, Czechia) extracted DNA from the Czech specimens of *P. granulatus* using the CTAB method (Doyle & Doyle 1987); and E.F. Malysheva extracted DNA from the Russian specimens following the manufacturing protocol of the Macherey-Nagel Nucleo-Spin Plant II Kit.

PCR AMPLIFICATION AND SEQUENCING—The ITS1–5.8S–ITS2 region from the ribosomal DNA was amplified and sequenced with primer pairs ITS1f–ITS4b or ITS1f–ITS4 (White & al. 1990; Gardes & Bruns 1993) and ITS5–ITS4 (White & al. 1990, Nikolcheva & Bärlocher 2004). PCR products were purified using the Thermo Scientific GeneJET Gel Extraction Kit or by precipitation with polyethylene glycol (10% PEG 6000 and 1.25 M NaCl in the precipitation mixture) and then sequenced with the Sanger method. Raw data were edited and assembled in Sequencher 4.7 and MEGA 6 (Tamura & al. 2013). The sequences generated were deposited in GenBank with corresponding accession numbers (TABLE 1).

PHYLOGENETIC RECONSTRUCTION—In addition to 12 ITS sequences newly generated for the study, 77 sequences including the outgroup *Pluteus chrysaegis* (Berk. & Broome) Petch were retrieved for phylogenetic reconstruction from GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>). The taxonomic identities of these sequences are given as they appear in GenBank (TABLE 1). The sequences were first aligned with the Muscle method/procedure (Edgar 2004) embedded in MEGA 6 and then corrected manually using the same program. The alignment was deposited in TreeBASE (S23054). Phylogenetic reconstructions for the dataset were performed with maximum likelihood (ML) and Bayesian (BA) analyses. Before the analyses, the best-fit

TABLE 1. Data for nrITS sequences used in the phylogenetic analyses.
The symbol ‘!’ indicates a type collection.

TAXON	GENBANK NUMBER (ITS)	COLLECTION (Herbarium)	GEOGRAPHIC ORIGIN, ISO code	SOURCE
<i>Pluteus chrysaegis</i>	JN603206	K13587	India	GenBank
<i>P. diana</i>	MH656433	629413 (PRM!)	CZ	This study
	MH656429	312978 (LE)	RU (European part)	This study
	FJ774076	213024 (LE)	RU (European part)	Malysheva & al. 2009
	MH656430	312950 (LE)	RU (European part)	This study
	MH656431	303485 (LE)	RU (European part)	This study
	MH656432	296318 (LE)	RU (European part)	This study
	MH656481	JHC99-030	DK	This study
<i>P. aff. dianne</i>	HM562055	AI209 (CUW)	ES	Justo & al. 2011
<i>P. cf. fernandezianus</i>	JQ065028	RSPF 0330	BR	GenBank
<i>P. fibrillosus</i>	KR022018	FK1903 (SP 417462)	BR	Menolli & al. 2015
<i>P. granulatus</i>	MH656434	HS11 (BRNM 807610)	CZ	This study
	MH656435	HS18_2 (BRNM 807611)	CZ	This study
	MG544915	OKA-374	TR	GenBank
	MG544916	OKA-349	TR	GenBank
	MG544914	OKA-101	TR	GenBank
	HM562048	AI203 (LOU)	ES	Justo & al. 2011
	FJ774086	212990 (LE)	RU (European part)	Malysheva & al. 2009
<i>P. heteromarginatus</i>	KR022008	AJ618	US (NY)	Menolli & al. 2015
<i>P. longistriatus</i>	HM562058	AJ172 (MICH)	US (FL)	Justo & al. 2011
	HM562082	Mimis309203 (SIU)	US (MO)	Justo & al. 2011
	MH211798	61188 (FLAS-F)	US (FL)	GenBank
	MF161220	BHT-F334b (FH)	US (MA)	GenBank
	KM052568	ASIS24529	KR	GenBank
	KX216355	312951 (LE)	RU (Far East)	Malysheva & al. 2016
	MH211936	61504 (FLAS-F)	US (FL)	GenBank
	KY777367	068931 (TENN)	US (TN)	GenBank
	HM562172	394386 (SP)	BR	Justo & al. 2011

TAXON	GENBANK NUMBER (ITS)	COLLECTION (Herbarium)	GEOGRAPHIC ORIGIN, ISO code	SOURCE
<i>P. plautus</i>	HM562158	393700 (SP)	BR	Justo & al. 2011
	HM562149	394004 (SP)	BR	Justo & al. 2011
	KU953374	-	IT	GenBank
	KT695338	BIOUG24046-H01	CA	GenBank
	MG544917	OKA-470	TR	GenBank
	MG544918	OKA-354	TR	GenBank
	KC581304	F23774 (UBC)	CA	GenBank
	KF306033	1859501 (UC)	CA	GenBank
	KX216322	303680 (LE)	US (CA)	GenBank
	KR022015	AJ227	RU (South Siberia)	Malysheva & al. 2016
<i>P. aff. plautus</i>	KR022014	A5058325	ES	Menolli & al. 2015
	KR022016	AJ597	US (NY)	Menolli & al. 2015
	KR022026	ACaballero 783	ES	Menolli & al. 2015
	KR022017	163299 (MO)	US (CA)	Menolli & al. 2015
	KR022025	AJ226	ES	Menolli & al. 2015
	MH656436	HS9 (BRNM 807612)	CZ	This study
	MH656437	HS18_6 (BRNM 807613)	CZ	This study
	KJ146724	F23908 (UBC)	CA	GenBank
	MH656438	682743 (PRM1)	CZ	This study
	MH656480	JHC04-298	SE	This study
<i>P. punctatus</i>	KF306034	1859499 (UC)	US (CA)	GenBank
	MG544921	OKA-388	TR	GenBank
	MG544920	OKA-430	TR	GenBank
	MG544919	OKA-362	TR	GenBank
	KR022022	18725 (LOU)	ES	Menolli & al. 2015
	FJ774080	227534 (LE)	RU (European part)	Malysheva & al. 2009
	KX216353	312914 (LE)	RU (European part)	Malysheva & al. 2016
	KR022021	AJ870	ES	Menolli & al. 2015
	KR022023	GM2551	ES	Menolli & al. 2015
	KR022024	FMateo s. n.	ES	Menolli & al. 2015
<i>P. romellii</i>	MF437007	20150903-15 (SFC)	KR	GenBank
<i>P. semibulbosus</i>				

TAXON	GENBANK NUMBER (ITS)	COLLECTION (Herbarium)	GEOGRAPHIC ORIGIN, ISO code	SOURCE
<i>P. semibulbosus</i> (continued)	KF668315	ASIS22533	KR	GenBank
<i>P. aff. semibulbosus</i>	MG544922	OKA-146	TR	GenBank
<i>P. cf. semibulbosus</i>	HM562090	F12393 (TNS)	JP	Justo & al. 2011
<i>Pluteus</i> sp.	KR022020	A5058211	ES	Menolli & al. 2015
	KC147672	1861124 (UC)	US (CA)	GenBank
	KR022009	93671 (MO)	US (OR)	Menolli & al. 2015
	KR022012	AJ594	US (NY)	Menolli & al. 2015
	KR022013	Miettinen15459	FI	Menolli & al. 2015
	KR022011	AJ606	US (NY)	Menolli & al. 2015
	KR022010	AJ621	US (NY)	Menolli & al. 2015
	KU131672	107524 (PDD)	NZ	GenBank
	KU131673	107527 (PDD)	NZ	GenBank
	KU131674	107530 (PDD)	NZ	GenBank
	KU131675	107529 (PDD)	NZ	GenBank
	KR022019	NMJ193	BR	Menolli & al. 2015
	KC147677	1861231 (UC)	US (CA)	GenBank
	KU131671	107526 (PDD)	NZ	GenBank
	KU131670	107525 (PDD)	NZ	GenBank
	KU131669	107523 (PDD)	NZ	GenBank
	KU131676	107528 (PDD)	NZ	GenBank
	KY352653	055370 (TENNI)	AR	GenBank
	KR022028	AJ470	US (VI)	Menolli & al. 2015
	KF306015	1999302 (UC)	US (CA)	GenBank
<i>P. velutinus</i>	KR022027	FK1889	BR	Menolli & al. 2015
	HM562114	F12365 (TNS)	JP	Justo & al. 2011
	HM562127	F12372 (TNS)	JP	Justo & al. 2011
	JN603205	12851 (K)	IN	Pradeep & al. 2012
	KX216340	303693 (1E)	RU (South Siberia)	Malysheva & al. 2016
	MG576118	29375 (MCVE)	IT	GenBank
Uncultured fungus clone	HQ257439	TSBF1_52	BR	GenBank

substitution model for the alignment was estimated based on the Akaike Information Criterion (AIC) using the FindModel web server (<http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>). Both ML and BA analyses employed the GTR model. ML analysis was run on the PhyML server, v. 3.0 (<http://www.atgc-montpellier.fr/phyml/>), with one hundred rapid bootstrap replicates. BA was performed using the MrBayes 3.2.5 software (Ronquist & al. 2012) for two independent runs, each with 7 million generations with sampling every 100 generations, under described model and four chains. To quickly diagnose convergence of MCMC analyses and to obtain estimates of the posterior distribution of parameter values, Tracer v1.6 was used (Rambaut & al. 2014). Bootstrap (BS) values $\geq 70\%$ and posterior probability (PP) values ≥ 0.95 are considered significant.

Results

Molecular phylogeny

The dataset comprises 88 sequences of *Pluteus* sect. *Hispidoderma* and one outgroup sequence (*P. chrysaegis*) and consists of 693 characters (with gaps). The overall topologies of the ML and BA trees are substantially the same.

The *P. diana*e and *P. punctatus* clades received high statistical support in both analyses. All sequenced collections of *P. diana*e appeared in a single clade in the phylogenetic tree (FIG. 1), including the sequence generated from the holotype collection. Genetic distance between these collections is less than 0.5%. One collection from Spain (AJ209) that appeared extremely close to the *P. diana*e clade but differed in seven nucleotide positions (and with a genetic distance from other collections ca. 1%) is provisionally named *Pluteus* aff. *diana*e.

Collections assigned to the *P. plautus* complex in the sense of Vellinga & Schreurs (1985) did not form a monophyletic clade (FIG. 1). For the time being, we have chosen to assign the published names only to the clades corresponding to *P. granulatus*, *P. longistriatus*, *P. semibulbosus*, and *P. velutinus* C.K. Pradeep & al. The other six species sampled here and belonging to the *P. plautus* complex are labelled simply *Pluteus* sp. I, II, III, IV, V, and VI. Work is currently underway to determine which clade should bear the name *P. plautus* and to designate a type that would stabilize the usage of the name.

Taxonomy

*Pluteus diana*e Pilát, Česká Mykol. 22(3): 171 (1968)

FIGS 2, 3, 6a,b,d-f

ORIGINAL DESCRIPTION. "Pileus 50–70 mm diam., regulariter orbicularis, adultus plane convexus vel planus, cacumine minime rugoso-reticulatus et ibi tinctu debili luteo-brunneo, ceterum albus, margine ad dimidium radii rimosus, ceterum laevis glaberque, cutícula marginem in forma membranae tenuissimae superanti, exsiccatus albus tinctu debili sordide isabellino. Lamellae liberae, sat latae et ventricosae, novae



albae, adultae albido-salmoneae. Stipes 50–60 × 6–7 mm, albus, minime longitudinaliter rugosus, subcylindraceus, deorsum paulum incrassatus basique truncata ad lignum putridum insidens, parte tertia basali haud raro minime disperse obscurius fibrilloso-subsquamosus.

“Carposoma, praecipue trama lamellarum et cutis pilei ex hyphis dimiticis, tenuiter tunicatis hyalinis, 4–8 μ crassis et hyphis crassius vel crasse tunicatis, 5–8 μ crassis, conspecte curvatis et haud raro tinctu debili luteolo conspectis, irregulariter et in ángulo recto curvatis et ramosis, parum septatis. Cutis pilei ex hyphis similibus et ex finibus hypharum clavato-saccatis (pileocystidiis) tenuiter tunicatis, hyalinis, decumbentibus, 60–100 × 14–25 μ magnis. Metuloideis crasse tunicatis corniculatisque in hymenio absentibus. Cheilocystidia in acie lamellarum copiosa, ovoidea, saccata vel sublageniformia, tenuiter tunicata, hyalina, 25–60 × 12–25 μ. Sporae globoso-ovoideae, subsalmoneae, laeves, apiculo parvo deflexo praeditae, 7.5–9 × 5–6.5 μ.”

HOLOTYPE—Czechoslovakia (currently Czechia), Rozvadov, Diana Nature reserve, in primeval forest, lying rotten trunk of *Fagus sylvatica* L. infected by *Fomes fomentarius* (L.) Fr., 18. VII. 1967 leg. et det. A. Pilát (PRM 629413).

TYPE REVISION. Basidiospores [1/1/30] (6.0–)6.5–8.5(–9.5) × 5.0–6.5(–7.0) μm, avl × avw = 7.2 × 6.3 μm, Q = 1.00–1.40(–1.60), avQ = 1.16, globose, subglobose or broadly ellipsoid, rarely ellipsoid. Basidia (18–)21–29(–32) × 7–9(–11) μm, tetrasterigmate, narrowly clavate to subcylindrical or subutriform, colourless. Pleurocystidia moderately abundant, (32–)35–82(–90) × (13–)15–26(–32) μm, fusiform, lageniform, less frequently utriform, usually with a ≤15 μm (very rarely ≤35 μm) long narrowed apex and 3.0–15.0 μm long pedicel, thin-walled, colourless. Lamellar edges sterile. Cheilocystidia (25–)30–48(–62) × (12–)14.5–26 μm, narrowly to broadly clavate, narrowly ventricose, scarcely sublageniform or cylindrical, thin-walled, colourless. Pileipellis a trichoderm, terminal elements 55–180(–280) × 14–24 μm, very variable in size, sometimes in similarly sized tufts (more often smaller than larger-sized elements), narrowly clavate to clavate, sometimes with a narrowed or strangled apex, sometimes with pale ochre intracellular pigment. Branched hyphae present in the subpileipellis. Stipitipellis a cutis of 4.0–12.0(–18.0) μm diam. cylindrical colourless hyphae. Caulocystidia in tufts, (30–)45–75(–82) × (9–)12–17.5(–20) μm, cylindrical or narrowly clavate, rarely with short obtuse rostrum, thin-walled, colourless or with very pale intracellular pigment. Clamp connections absent in all studied tissues.

FIG. 1. Best tree from Maximum likelihood analysis for the nrITS dataset showing some lineages within *Pluteus* sect. *Hispiderma*. For sequences retrieved from GenBank the corresponding accession numbers are given. The newly generated sequences are indicated with the collection numbers (in parentheses). Support values given above the branches are BS ≥70% / PP ≥0.95. Scale bar shows expected changes per site.

Characteristics of the type locality and type specimen

Diana Nature Reserve is a protected area in western Czechia close to the German border and situated in the Český les mountains near the village of Rozvadov at 500–532 m a.s.l. (central point: 49°37'57"N 12°34'43"E). The Český les mountain range belongs to the Bohemian massif Mesophyticum (Skalický 1988) with a ca. 7–8 °C mean annual temperature and 700–800 mm mean annual precipitation. Climatically, this region is classified as mildly warm zone (MT3 on the Quitt scale, Vrška & al. 2012). The reserve comprises predominantly near-natural herb-rich beech forests, in particular the *Dentario enneaphylli-Fagetum* association in an advanced stage of degradation (Zahradnický & Mackovčín 2004). Based on their mensurational surveys, Vrška & al. (2012) detected an extensive disturbance in a part of the reserve, thus establishing that Diana is not now a natural forest. The protected area comprises a 300-year old forest of *Tilia cordata*, *Quercus robur*, and *Picea abies*. Pilát (1968), who collected the holotype collection from a rotting trunk of *Fagus sylvatica* lying on the ground, stated that he collected and photographed two basidiomata. However, only one basidiocarp is shown in the photograph (Pilát 1968: 172). The original material is preserved in dried form and in good condition in the herbarium of the Mycological Department of the National Museum in Prague (PRM 629413!).

Additional collections studied

Pileus 20–120 mm in diam., broadly conical, convex to applanate, sometimes with broad low umbo; creamy-grey or cinnamon buff, greyish-brown or brown; drying $\pm$ whitish-grey, surface felty or covered with white appressed hairs; in some specimens irregularly wrinkled in centre, in some specimens striate at margin. Lamellae pink with concolorous edges. Stipe 30–70(–100) $\times$ 2.5–10 mm, broadened towards base or bulbous; pure white, whitish, or yellowish; longitudinally striate, whitish floccose to granulose-pruinose. Smell indistinct or pleasant, sweetish-spicy.

Basidiospores [5/5/150] 5.5–8.0(–9.0) $\times$ 4.5–6.5(–6.8) μm , $\text{avl} \times \text{avw} = 7.2 \times 5.5 \mu\text{m}$, $Q = (1.10\text{--})1.17\text{--}1.46$, $\text{av}Q = 1.30$, broadly ellipsoid to ellipsoid or ovoid, rarely subglobose. Basidia 25–37 $\times$ 8–12 μm , tetrasterigmate. Pleurocystidia abundant, 54–86(–103) $\times$ (14–)18–27(–34) μm , mostly (broadly) lageniform, (narrowly) utriform, or fusiform, commonly with a small apical excrescence, more rarely with more than one on the same cystidium, colourless. Cheilocystidia abundant, forming a sterile layer, very variable in size, (41–)52–95(–115) $\times$ (14–)17–27(–32) μm , narrowly

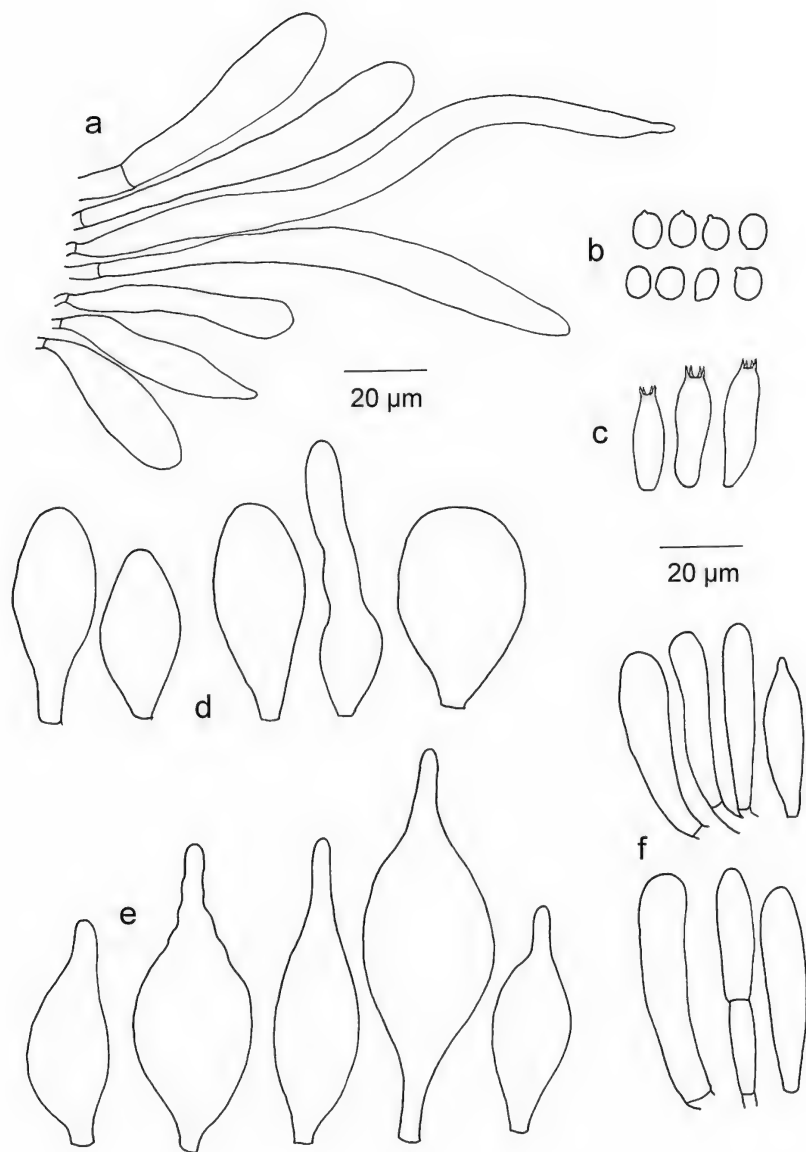


FIG. 2. *Pluteus diana* (holotype, PRM 629413): a. pileipellis elements; b. basidiospores; c. basidia; d. cheilocystidia; e. pleurocystidia; f. caulocystidia. (del. H. Ševčíková).

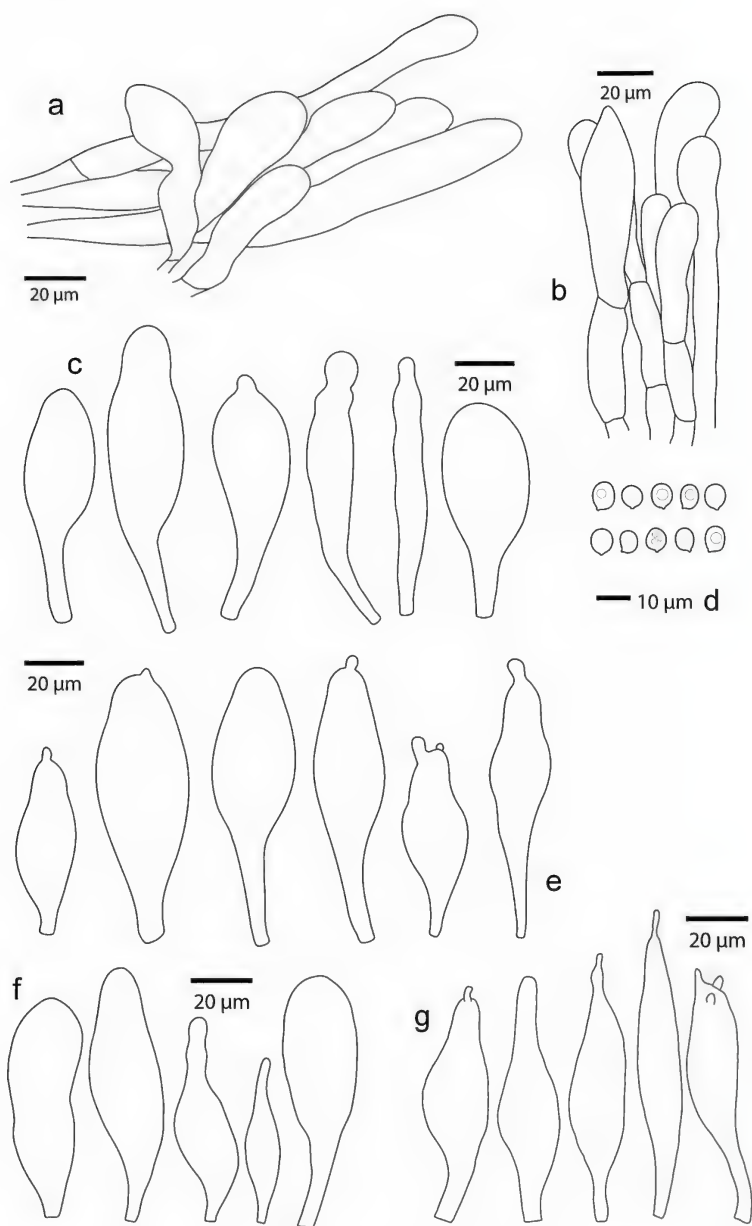


FIG. 3. *Pluteus diana* (LE312950): a. pileipellis elements; b. caulocystidia; c. cheilocystidia; d. basidiospores; e. pleurocystidia. (del. E.F. Malysheva); (JHC 99_30): f. cheilocystidia; g. pleurocystidia. (del. A Justo).

to broadly clavate, narrowly utriform to utriform, ovoid or cylindrical, lageniform, pedicellate, some with single apical papilla, thin- or slightly thick-walled. Pileipellis a trichoderm, terminal elements (50–)79–125(–220) $\times$ 14–36 μ m, clavate, utriform or cylindrical, some with tapering apex. Caulocystidia in clusters, 43–140 $\times$ 14–27 μ m; narrowly clavate, narrowly utriform, narrowly fusiform, or narrowly lageniform; thin-walled, colourless. Clamp connections absent.

COLLECTIONS STUDIED—DENMARK, SJÆLLAND, Næsbyholm Storskov [SW of Ringsted], 55°22'26"N, 11°35'50"E, on fallen log of *Fagus sylvatica*, 24 VIII 1999, leg. J. Heilmann-Clausen (JHC99-030, as *P. cf. depauperatus*). RUSSIA: SAMARA REGION, Zhiguli State Nature Reserve, broadleaved forest (*Tilia cordata*, *Acer platanoides*), on fallen trunk of deciduous tree, 9 VII 2003, leg. E. Malysheva (LE 312950, as *Pluteus plautus*); broadleaved forest, on fallen trunk of deciduous tree, 27 VIII 2001, leg. E. Malysheva (LE 312978, as *Pluteus plautus*); MOSCOW REGION, Zvenigorod Biological Station of Moscow State University, 55°41'00"N 36°43'00"E, mixed forest, on fallen trunk of *Populus tremula*, 19 VI 2013, leg. E. Voronina (LE 296318, as *Pluteus plautus*); *Picea* forest (with *Pinus* and *Betula*), on decayed deciduous tree, 10 VI 2014, leg. E. Voronina (LE 303485, as *Pluteus plautus*).

COMMENTS—The Danish collection was from a somewhat open, seminatural, deciduous woodland dominated by *Fagus sylvatica* and on a north-facing slope facing the river Susåen. The annual temperature of the site averages 8.6–8.8 °C, and the annual precipitation averages 600–700 mm (Wang 2013). The Russian collection sites lie in the submontane belt and mountain territory (Zhiguli State Nature Reserve) and plains (Moscow State University Zvenigorod Biological Station) with the annual temperature averaging 10.3 °C and the total annual precipitation averaging 904.4 mm (http://www.earthonlinemedia.com/ipg/outlines/climates_humid_continental.html).

Pluteus punctatus Wichanský, Mykol. Sborn. 49(1–2): 1 (1972)

Figs 4, 5, 6C

ORIGINAL DESCRIPTION. "Pileus tenuiter carnosus, 5.5 cm diam., pallide griseo-brunneolus, late convexus, dimidio squamulis brunneis minutis flocculosis punctiformibus ad marginem absentibus obtextus. Lamellae confertae, ventricosae usque 10 mm latae, remotae, albidae, dein incarnatae. Stipes 4 cm longus atque 8 mm crassus, solidus, cylindraceus, ad basim paulum incrassatus, albus, nudo apice excepto aquamulis brunneis, minutis, flocculosis dense punctatus. Cystidia varie formata, ellipsoideo- vel ovato-clavata, nonnullae ventricosae fusiformia. Sporae late ellipsoideae, 7–8.5 $\times$ 5.5–6.5 μ m. Cellulae cuticulae pilei cylindricae, longissimae, 13–26 μ m crassae. Caro pilei et stipitis alba. Odor et sapor nullae."

HOLOTYPUS—Carposoma solitarium do. Frant. Fuchs 4. X. 1969 ad codicem *Populi albae* in Řevnice (Czechoslovakia [currently Czechia], Bohemia centralis) legit et mihi donavit. Typus in herbario Musei nationalis Pragae asservatur (PRM 682743).

TYPE REVISION. Basidiospores [1/1/30] (5.0–)7.0–8.5(–9.5) $\times$ 5.0–7.0(–7.5) μm , $\text{avl} \times \text{avw} = 7.6 \times 6.5 \mu\text{m}$, $Q = (1.00\text{--})1.05\text{--}1.33(1.40)$, $\text{av}Q = 1.2$, subglobose or broadly ellipsoid, rarely globose or ellipsoid. Basidia (18–)22–28 (–30) $\times$ 8–10(–12) μm , tetrasterigmate, rarely bisterigmate, narrowly clavate to subcylindrical or subutriform, colourless. Pleurocystidia scattered, 28–65 $\times$ (13–)15–26(–32) μm , fusiform, lageniform, less frequently utriform, often with $\leq 9 \mu\text{m}$ long obtuse apex, sometimes with $\leq 13 \mu\text{m}$ long pedicel, thin-walled, colourless. Lamellar edges sterile. Cheilocystidia abundant (28–)44–65 (–86) $\times$ (14–)16–33 μm , broadly clavate, narrowly ventricose, fusiform to broadly fusiform, obovoid, scarcely sublageniform, sometimes with $\leq 12 \mu\text{m}$ long pedicel, rarely with a short rounded apex, thin-walled, hyaline. Pileipellis a trichoderm, terminal elements 55–280(–380) $\times$ 13–26(–38) μm , variable in size, narrowly clavate to clavate, sometimes with a narrowed or slightly strangled apex, with or without colourless or with pale brown intracellular pigment. Stipitipellis a cutis of 5.0–11.0(–16.0) μm diam. cylindrical hyaline hyphae. Caulocystidia solitary or in small tufts, scattered, (24–)28–60 $\times$ 10–25 μm , cylindrical or narrowly clavate, obovoid with short pedicel or obfusiform, thin-walled, with or without very pale brown intracellular pigment. Clamp connections absent in all studied tissues.

Characteristics of the type locality and type specimen

Řevnice is a town situated about 10 km southwest of the Prague city limits on the Berounka river, lying at 200 m a.s.l. (surrounded by ca. 500 m hills (central point: 49°54'50"N 14°14'09"E). The area belongs to the Bohemian Massif, Thermophyticum (Skalický 1988) with annual averages of 8.5–9 °C and 504–527 mm precipitation (Merkel 2018, Tolasz 2007). Wichanský (1972) did not describe the ecology in detail, citing only the growth on a *Populus* sp. stump. Therefore it is unclear whether the type specimen was found in a semi-natural alluvial woodland, a disturbed stand, or an ornamental tree in the town.

Wichanský (1972) mentions only one basidiocarp, and no other original material exists. This basidiocarp is preserved as a holotype in the herbarium of the Mycological Department of the National Museum in Prague (PRM 682743 contains one dried basidiocarp in good condition).

Additional collection studied

Pileus scales greyish-brown in centre, outwards cream to ochraceous, ≤ 25 mm diam. (dried specimen). Lamellae free, 1–2 tiers of lamellulae, crowded, lamellar edge concolorous. Stipe 32 $\times$ 2 mm (dried specimen), cylindrical, broadened towards base, finely pruinose. Smell and taste not recorded.

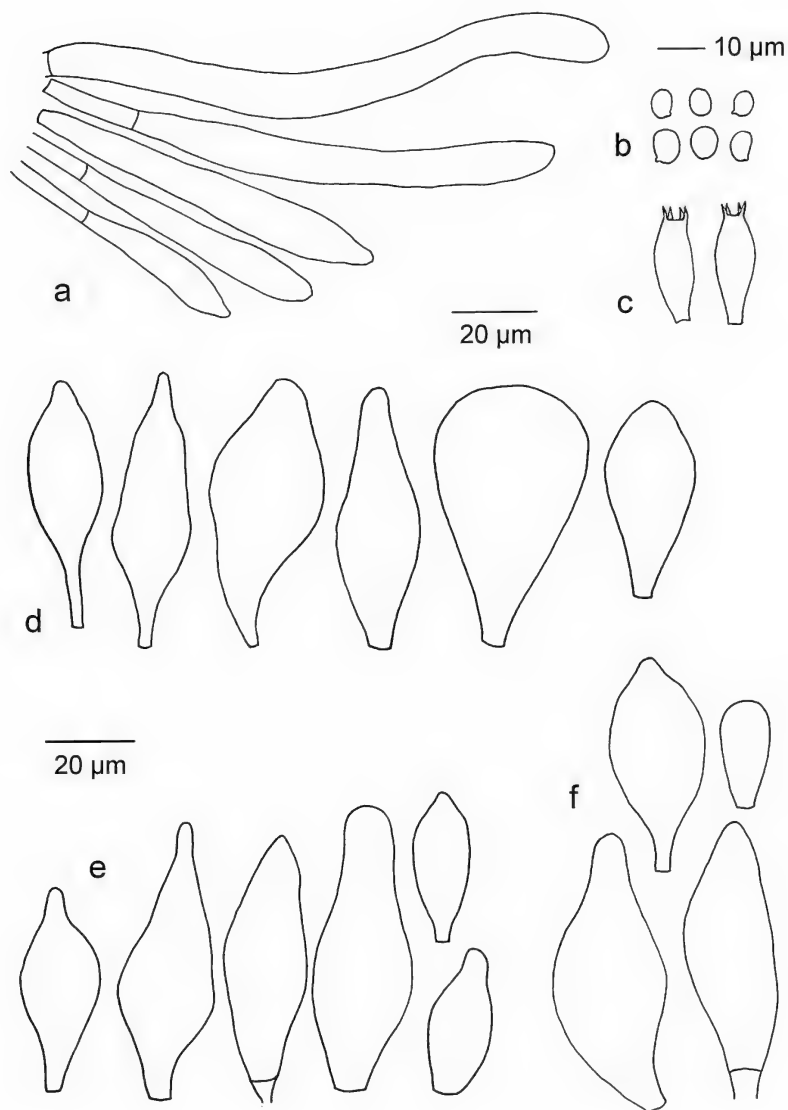


FIG. 4. *Pluteus punctatus* (holotype, PRM 682743): a. pileipellis elements; b. basidiospores; c. basidia; d. cheilocystidia; e. pleurocystidia; f. caulocystidia.

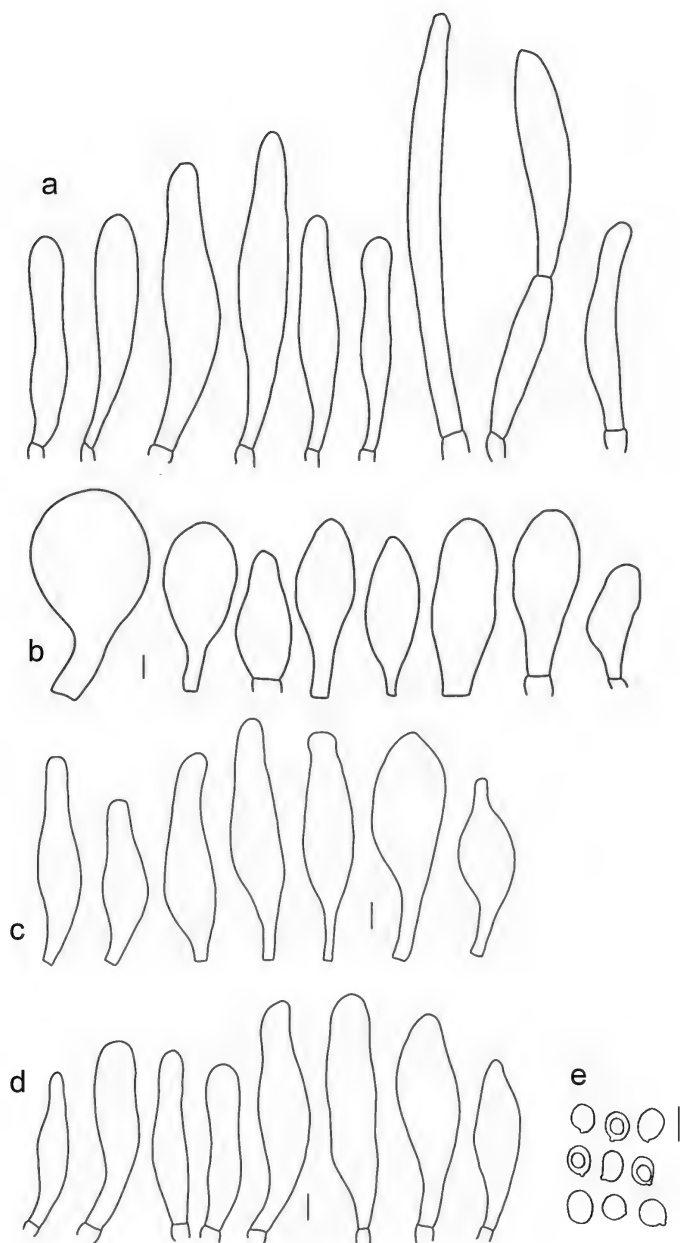


FIG. 5. *Pluteus punctatus* (JHC 04_298): a. pileipellis elements; b. cheilocystidia; c. pleurocystidia; d. caulocystidia. (del. A. Justo). e. spores. (del. H. Ševčíková). Scale bars = 10 μ m.

Basidiospores [1/1/30] $6.5\text{--}8.5 \times 4.5\text{--}7.0\ \mu\text{m}$, $\text{avl} \times \text{avw} = 7.3 \times 5.8\ \mu\text{m}$, $Q = (1.10\text{--})1.15\text{--}1.39$, $\text{av}Q = 1.27$, broadly ellipsoid to ellipsoid, rarely subglobose. Basidia $24\text{--}32 \times 7\text{--}11\ \mu\text{m}$, tetrasterigmate. Pleurocystidia abundant, $50\text{--}80(-100) \times 17\text{--}32(-44)\ \mu\text{m}$, mostly lageniform, narrowly utriform or fusiform; hyaline. Cheilocystidia abundant, $58\text{--}106 \times 17\text{--}46\ \mu\text{m}$, mostly clavate, narrowly utriform or fusiform; hyaline. Pileipellis a trichoderm, terminal elements $85\text{--}250 \times 15\text{--}27(-35)\ \mu\text{m}$, (narrowly) clavate, narrowly utriform, fusiform, or cylindrical. Caulocystidia abundant, isolated or in loosely arranged clusters; $61\text{--}100 \times 17\text{--}31\ \mu\text{m}$, narrowly clavate, narrowly utriform, lageniform, or fusiform; hyaline. Clamp connections absent in all studied tissues.

COLLECTION STUDIED: SWEDEN, HALLAND, Dömostorp, Musikedalen, Vallåsen, $56^{\circ}22'17''\text{N}$ $13^{\circ}05'45''\text{E}$, on *Fagus* log, 5 X 2004, leg. Jacob Heilmann-Clausen (JHC 04-298, originally as *P. cf. depauperatus*).

COMMENTS—The Swedish specimen was collected from a fallen beech log in a small (4.4 ha) almost pure beech stand containing a considerable amount of dead wood, often in sunlit gaps. The ~210-year-old stand is rather even-aged and part of the larger (110 ha) Musikedalen nature reserve, protected since 2010. The stand has been without active management of the living trees since 1946 and under strict protection since 1996 (Länstyrelsen Halland 2010). The forest lies at 180 m a.s.l. adjacent to a larger bog area and elsewhere surrounded by spruce plantations. The climate is temperate with an Atlantic influence with an annual average precipitation of 1000–1100 mm (SMHI 2018a) and ca. 7 °C temperature (SMHI 2018b).

Distribution & ecology

*Pluteus diana*e was previously known only from its type locality in Czechia. Our study extends the known distribution to Denmark and Russia. In addition, phylogenetically identical collections are reported from Turkey (GenBank Acc. No. MG544918.1 and MG544917.1, as *Pluteus plautus* (Kaygusuz & al. 2019). *Pluteus diana*e can now be said to occur through northern, central, and eastern Europe into Turkish Asia. Climatically, the European collection sites lie in the temperate continental zone (SMHI 2018b, Tolasz 2007) with precipitation averaging 600–900 mm annually (Merkel 2018, Wang 2013). The sites are located from the lowlands to the mountains. The Turkish collections were found near mountains at 250–850 m elevations in northwest Turkey in areas of regular and high rainfall (Kaygusuz & al. 2019). *Pluteus diana*e, which grows on decaying trunks of deciduous trees, is known from *Fagus* spp., *Populus tremula*, and a fallen trunk of an unidentified deciduous tree.

Pluteus punctatus was also known only from its type locality in Czechia. The Swedish collection adds important ecological and distributional data. Its collection sites lie in the European temperate area (SMHI 2018b, Tolasz 2007) with a mean annual precipitation of 504–1100 mm (Merkel 2018, SMHI 2018a). Both sites are located in the lowlands. *Pluteus punctatus*, which grows on dead wood of deciduous trees, has been collected from a *Populus* sp. stump and fallen *Fagus sylvatica* trunk.

OTHER STUDIED COLLECTIONS OF SIMILAR TAXA:

Pluteus atriavellaneus: USA: TENNESSEE, Unicoi Co., Unaka Springs, dead wood, 18–24 Aug. 1904, W. A. Murrill 673 (NY, type).

Pluteus avellaneus: USA: NEW YORK, Essex Co., Lake Placid, Adirondacks, dead wood, 17–29 Jul. 1912, W. A. Murrill 91 (NY, type).

Pluteus compressipes: JAMAICA: Castleton Gardens, dead wood, wet and shaded, 15 Dec. 1908, W. A. Murrill 118 (NY, type).

Pluteus depauperatus: FRANCE: Château de La Grange, Yerres, stumps and trunks of *Fagus*, Aug. 1936 leg. & det. H. Romagnesi (PC, type).

Pluteus fibrillosus: USA: LOUISIANA, New Orleans, Chalmette, New Orleans, in soil in a wet thicket, 8 Sept. 1908, F. S. Earle 129 (NY, Type).

Pluteus fuliginosus: USA: NEW YORK, Essex Co., Lake Placid, Adirondacks, 17–29 Jul. 1912, white pine stump decayed, coniferous or mixed forest, W. A. Murrill 118 (NY, type).

Pluteus granulatus: CZECHIA: Kladeruby nad Oslavou, Vlčí kopec, cultivated spruce forest, on a rotten stump of *Picea abies*, 3 Oct. 2013 leg. & det. H. Ševčíková (BRNM 761707); Česká Třebová, Křivolík stream, on rotten stump of *Picea abies* lying in a stream, 15 Aug. 2017 leg. M. Mička, det. H. Ševčíková (BRNM 807610); Psáry, cultivated spruce forest, near a road, cavity of rotting stump of *Picea abies*, 20 Sept. 2015 leg. J. Herčík, det. H. Ševčíková (BRNM 807611). ITALY, probably Trentino, Val di Sole, rotten ? of *Abies* near meadow, Aug. 1882 leg. & det. G. Bresadola (S F14380 lectotype).

Pluteus hiatus: FRANCE: Oise, Lamorlaye, rotten deciduous stump (*Populus* sp.?) 10 Sept. 1946 leg. Romagnesi H.? (PC, type); Château de La Grange, Yerres, stumps of *Fagus*, Aug. 1936 leg. & det. H. Romagnesi (PC, herbarium of Romagnesi).

Pluteus inflatus: CZECHIA: Mnichovice, trunk of *Alnus* (*A. glutinosa* according to observations by H.Š.), Aug. 1944, leg. & det. J. Velenovský (PRM 154569, type).

Pluteus latifolius: USA: WASHINGTON, Seattle, on dead alder, 20 Oct. – 1 Nov. 1911, W. A. Murrill 510 (NY, type).

FIG. 6. *Pluteus diana*: a. (JHC 99_30) basidiomata (photo J. Heilmann-Clausen); b. (holotype, PRM 629413) dried basidioma (photo H. Ševčíková). *Pluteus punctatus* c. (holotype, PRM 682743): dried basidioma (photo H. Ševčíková). *Pluteus diana*: (LE312950): d. pleurocystidia; e. basidium with spores and pleurocystidia (photos E.F. Malysheva). f. (JHC 99_30). caulocystidium (photo H. Ševčíková). Scale bars: b–c = 1 cm, d–f = 20 µm.



Pluteus plautus sensu lato: CZECHIA: Babice, PR Čihadlo, *Fagetum*, fallen stem of *Fagus sylvatica*, 17 May 2017 leg. & det. H. Ševčíková (BRNM 807612, HS9); Valtice, Rendezvous National Nature Monument, fallen deciduous stem, 2017 leg. P. Včelička, det. H. Ševčíková (BRNM 807613, HS18_6).

Pluteus puberulus: CZECHIA: Choteč, Radotín valley, rotten stump of *Alnus* sp. (probably *A. glutinosa*), Aug. 1918, leg. & det. J. Velenovský (PRC, Velenovský collection, bottle 78 f, type).

General discussion

Taxonomy

*Pluteus diana*e was originally characterized by its large whitish pileus tinged slightly yellowish-brown at the centre and a whitish striate stipe subpruinose only in the lower part (Pilát 1968). However, all studied Russian collections with similar ITS sequence data are described as having a brown or greyish-brown pileus with a velvety surface or covered with white appressed hairs and a whitish or yellowish striate often granulose-pruinose stipe. Microscopically, Pilát (1968) emphasized the absence of metuloid cystidia with hooks but did not explicitly describe any other kinds of pleurocystidia. Our examination of the holotype (PRM 629413!) revealed (narrowly) lageniform or fusiform pleurocystidia with a narrowed apex and a pedicel (FIG. 2e), also found in all other studied collections (FIGS 3e, g; 6d–e). Pilát (1968) cited basidiospores measuring $7.5\text{--}9.0 \times 5.0\text{--}6.5 \mu\text{m}$, while our type revision showed a slightly wider range [$(6.0\text{--})6.5\text{--}8.5\text{--}(9.5) \times 5.0\text{--}6.5\text{--}(7.0) \mu\text{m}$] in concordance with the Russian collections. The Danish collection is morphologically similar to the type and Russian collections except for the scattered caulocystidia, apparently reflecting the rather poor condition of the dried material, as the macroscopical notes mention the stipe as being whitish floccose.

Although the Spanish collection AJ209 (Justo & al. 2011b) is phylogenetically close to *Pluteus diana*e, we maintain its identification as *Pluteus* aff. *diana*e based on its different ITS sequence and the following morphological differences from *P. diana*e: (i) smaller pilei (3.5–5 cm diam.); (ii) broadly ellipsoid to ellipsoid (rarely subglobose) and smaller basidiospores [$5.5\text{--}7.5 \times 4.4\text{--}6.2 \mu\text{m}$, $avl \times avw = 6.6 \times 5.3 \mu\text{m}$, $Q = (1.08) 1.17\text{--}1.40$, $avQ = 1.24$]; and (iii) pleurocystidia without apical excrescences.

Pluteus punctatus was described with a pale grey-brown pileus with dark-brown floccose squamules, a whitish stipe with brown tomentose squamules, and variably shaped cystidia (Wichanský 1972: 1). The pileus scales of the Swedish collection are grey-brown in centre, outwards cream to ochraceous. Our microscopical examination of the holotype (PRM 682743!) and

in concordance with the Swedish collection reveals striking fusiform, lageniform, or utriform pleurocystidia $\leq 80\ \mu\text{m}$ long (FIGS 4e, 5c) and caulocystidia not arranged in large tufts but isolated or in loosely arranged clusters (FIGS 4f, 5d).

Similar taxa

According to Pilát (1968), *Pluteus diana*e resembles *Pluteus petasatus* (Fr.) Gillet and *Pluteus pellitus* in having a large white pileus. However, these species belong to *Pluteus* sect. *Pluteus*, characterized by metuloid pleurocystidia and a cutis pileipellis.

Both *Pluteus diana*e and *P. punctatus* belong to the taxonomically complicated *P. plautus* complex. Different authors have interpreted the species in this complex in noticeably diverse ways. Whereas Citérin & Eyssartier (1998) mentioned about six species in Europe, Vellinga (1990) recognized only one broad species—*Pluteus plautus*—incorporating nine taxa described by Lasch (Fries 1838), Bresadola (1881, Schulzer 1885), Romagnesi (Kühner & Romagnesi 1953), Orton (1960, 1969), and Wichanský (1972). Other poorly known species of this complex were described by Velenovský (1921) and Pilát (1968). Several additional species in the complex described from North America (Murrill 1917) may well also occur in Europe. Below we provide an overview of names published in this complex in Europe and North America, discussing their similarity to *Pluteus diana*e and *P. punctatus* so as to establish a basis for future taxonomic work in this species complex.

Pluteus plautus (Weinmann 1836: 394), was originally characterized by an alutaceous to fuliginous pileus with a velvety brown to blackish brown stipe and stipe context. Gillet (1876: 394) interpreted it as a small species without specifying basidioma dimensions. *Pluteus punctatus* was originally described by Wichanský (1972) as macroscopically similar to *P. plautus*, but it differs from *P. punctatus* (and *P. diana*e) in having a darker stipe and brown stipe context. Based on Weinmann's type description and our own field experience, we consider the dark colour of the context (especially in the stipe) an important diagnostic character of *P. plautus* sensu stricto. As *P. plautus* is interpreted differently by several agaricologists (e.g. Orton 1986, Vellinga 1990, Citérin & Eyssartier 1998), a neotypification is needed.

Following the tradition of Kühner & Romagnesi (1953), *Pluteus semibulbosus* (Lasch) Quél. also belongs to the *P. plautus* complex. It was originally characterized as a small whitish species with a softly atomate,

sulcate pileus and pubescent stipe with a distinctly bulbous base (Fries 1838). Lasch (in Fries 1838) did not mention basidioma dimensions, but Saccardo (1887: 674) mentioned a 13 mm broad pileus and 25 mm long stipe. Orton (1960: 349, 1986: 55) interpreted *P. semibulbosus* as belonging to *P.* subsect. *Eucellulodermini*, and published the name *Pluteus boudieri* P.D. Orton for *P. semibulbosus* sensu Boudier, Kühner & Romagnesi. However, for us, the original description of the stipe as pubescent strongly supports *P. semibulbosus* in *P.* sect. *Hispidoderma* and within the *P. plautus* complex. This interpretation would place the name *P. boudieri* in synonymy with *P. semibulbosus*. Recent collections referred to *P. semibulbosus* by us demonstrate that this broad morphological species concept corresponds to a polyphyletic group (unpublished data) and that further studies, including the selection of a type for *P. semibulbosus*, are needed. Even in its broad concept *Pluteus semibulbosus* can be distinguished from *P. punctatus* and *P. diana*e at least by its smaller basidiomata and bulbous stipe bases, while pale colouration is more diagnostic of *P. punctatus*.

Pluteus aestivus Velenovský (1921: 607) was described as similar to *P. semibulbosus* but having cuneiform-ellipsoid, non-translucent brown basidiospores, suggesting it belongs in a different genus than *Pluteus*. As original material is no longer extant, the name is impossible to interpret exactly, and we consider it a nomen dubium.

Pluteus candidus Patouillard (1887: 156) was described as a small species with a white, non-striate, silky pileus up to 10 mm broad, a pale thin stipe, and fusiform cystidia. It differs from both *P. diana*e and *P. punctatus* by its smaller basidiomata and silky pileus, and *P. punctatus* is further distinguished by the darker pileus colour. *Pluteus candidus* probably belongs to the *P. semibulbosus* complex. A smooth non-striate pileus is an important diagnostic feature for *P. candidus*. Nonetheless, finding a holotype of *P. candidus* is important for future research.

Pluteus stylobates Velenovský (1921: 608) was described as a small whitish agaric with a ≤ 10 –15 mm broad white pileus with dark squamules and a discoid stipe base resembling *Mycena stylobates* (Pers.) P. Kumm. The species therefore seems to belong to the *P. semibulbosus* complex. Unfortunately the holotype (PRC, Velenovský collection, bottle no. 396), no longer exists (it dried up and was destroyed years ago). This taxon may be a good species, but neotypification is necessary. Both *P. diana*e and *P. punctatus* have larger basidiomata and lack a discoid stipe base, and *P. punctatus* differs also by the darker colours.

Pluteus gracilis (Bres.) J.E. Lange was originally described by Bresadola (Schulzer 1885: 134) as *P. pellitus* var. *gracilis* Bres. Lange (1936: 84) assigned this taxon to *P.* subsect. *Depauperati*. His description and painting (Lange 1936: tab. 71 E) showed a whitish to very pale ochre *Pluteus* with dirty brown squamules on the pileus and stipe, presumably belonging to the *P. plautus* complex. However, it is unclear based on which material Bresadola described this taxon as a variety of *Pluteus pellitus*. Until a type has been located, we find it difficult to interpret this taxon.

Pluteus depauperatus Romagn. (Kühner & Romagnesi 1956: 181) was described with an 18–50 mm broad, velvety dull pale brown or brownish grey-ochre pileus, distinctly striate at the margin and sometimes granulate in the centre. The stipe was described as white when young, but striped pruinose brown-saffron to brick-saffron in mature specimens (Kühner & Romagnesi 1953). The holotype of *P. depauperatus* (PC!) contains two envelopes with material. The envelope with the larger basidiocarp marked as the type is in a rather poor condition, with deformed or collapsed cystidia and irregular, probably deformed, basidiospores ($7.0\text{--}8.0 \times 4.0\text{--}5.0$ μm). The envelope with the smaller basidiocarp is better preserved and its microcharacters agree with Romagnesi's original description (Kühner & Romagnesi 1953) and spores measuring $(5.0\text{--}) 6\text{--}6.5$ ($\text{--}7.0$) $\times 5.0\text{--}6.0$ μm , $\text{avl} \times \text{avw} = 6.33 \times 5.43$ μm . Pilát (1968), who mentioned the similarity of *P. diana*e with *P. depauperatus*, distinguished the latter by its pale brown, grey-brown or saffron-brown pileus, smaller basidiospores (see above), and an odor resembling *Lepiota cristata* (Bolton) P. Kumm. or *Scleroderma* Pers. The saffron-tinged mature stipe should also help separate *P. depauperatus* from both *P. diana*e and *P. punctatus*. Moreover, in all observed collections, *P. punctatus* lacks a striate pileus margin. *Pluteus depauperatus* seems to represent a good species, but verification by holotype DNA sequencing is needed.

Pluteus hiatus Romagn. (Kühner & Romagnesi 1953: 421, as nom. nov., validly published in 1956: 182 with the addition of the Latin diagnosis) was originally described as having a dirty brown, soon fading pileus with a *Coprinus*-like membranaceous striate margin, a satin white to pale brown (more at the base) stipe, and refractive utriform or lageniform pleurocystidia with pale brown vacuoles. Our holotype revision (PC!) confirmed that the pleurocystidia are refractive, narrowly to broadly (sub)lageniform to fusiform (rarely subutriform to utriform), and only rarely with very pale brown guttules. However, it is possible that brown guttulae fade with time

in exsiccates. Romagnesi's measurements (in Kühner & Romagnesi 1953) of subglobose basidiospores at $5.7\text{--}6.2(-7.5) \times 5\text{--}6.5\text{ }\mu\text{m}$ agree with our type study. *Pluteus diana*e and *P. punctatus* differ from *P. hiatus* by having a thicker-fleshed pileus with a less striate and non-*Coprinopsis*-like margin and possessing hyaline non-refractive pleurocystidia.

Pluteus punctipes Orton (1960: 361) was described as having relatively small to moderately large basidiomata with a sepia or umber to vandyke brown coloured pileus and sepia to dirty yellowish brown minute fibrillose scales on both pileus and stipe. Its possession of large ($\leq 100 \times 30\text{ }\mu\text{m}$) lageniform pleurocystidia with a short to long neck and with a brown vacuole is macroscopically expressed in some places as slightly dark brown lamellae. Orton (1960) also mentioned narrow clamped hyphae below cylindrical-fusiform pileipellis elements. The species seems to be close to *P. plautus* s. str. *Pluteus diana*e and *P. punctatus* differ in their hyaline and shorter pleurocystidia. Further studies and sequencing of the type are needed to clear up the taxonomic position and delimitation of *P. punctipes*.

Pluteus dryophiloides Orton (1969: 115) was originally described as having colours similar to *Gymnopus dryophilus* (Bull.) Murrill with a whitish or buff coloured stipe; a pileipellis with relatively short (60–152 μm) terminal cells; and vesiculose-fusiform, broadly pyriform, or broadly lageniform pleurocystidia sometimes terminating in solitary short pimples. *Pluteus diana*e and *P. punctatus* differ by their duller pileus colours, longer pileipellis terminal elements, and different pleurocystidia.

Pluteus granulatus Bresadola (1881: 10) was described as having a brown-reddish granulate pileus and a whitish, finely furfuraceous stipe with a yellowish furfuraceous base; the species was described as growing on coniferous wood, and that substrate may indeed be an important character for separating *P. granulatus* from other species in the *P. plautus* group. We consider collections HS11 (BRNM 807610) and HS18_2 (BRNM 807611) (Fig. 1) to represent *P. granulatus* in its original sense. Unfortunately, Kühner & Romagnesi (1956) cited *P. granulatus* as growing on *Fagus sylvatica*, which caused subsequent taxonomic confusion. In GenBank, several collections assigned to *Pluteus granulatus* were indicated as growing on *Fagus orientalis*. Our ITS sequences (HS9 and HS18_6), molecularly similar to other collections named *P. granulatus* from *Fagus sylvatica*, do not represent *P. granulatus*. These collections are here referred to *Pluteus* sp. VI (Fig. 1) pending further clarification of the *P. plautus* complex. *Pluteus diana*e and *P. punctatus* differ from *P. granulatus* by growth on deciduous wood and the

lack of a reddish tinge and distinct granules on the pileus, with the pileus of *Pluteus diana*e usually paler. Microscopically, the lectotype (S F14380!) of *P. granulatus* possesses lageniform (rarely fusiform) pleurocystidia that lack the apical excrescences, which are relatively frequent in *P. diana*e. Further, the pileipellis terminal elements are shorter and more uniform in size than in *P. punctatus* and *P. diana*e.

Pluteus puberulus Velenovský (1921: 607) was described as having a leathery, ochre, brown-streaked pileus that in places is almost squamulose, scaly, entirely ochre, or covered by small grains and a stipe that is grooved, densely velvety pubescent, and dirty yellowish. Velenovský (1921) also described yellowish cheilocystidia. The holotype is preserved in a bottle of Velenovský's solution (Fassatiová & al. 1994) in which yellow colours were said to fade (Velenovský (1921: 608). As the holotype (PRC, Velenovský collection, bottle 78 f!) contains only a part of the pileus in bad condition, determination of the identity of the preserved fungus is impossible and the taxonomic position of *P. puberulus* remains unclear.

Pluteus opponendus (Britzelm.) Sacc., originally described with a white pileus and stipe, might resemble *P. diana*e except for the significantly different basidiospores ($8\text{--}9 \times 4 \mu\text{m}$; Britzelmayer 1881: 136). *Pluteus opponendus* has an unclear taxonomical position.

Pluteus tiliaceus Velenovský (1921: 607), which was described with white to whitish colours similar to *P. opponendus*, is unique within the *P. plautus* complex by its small ($\sim 4 \mu\text{m}$ diam.) globose basidiospores, smooth, glabrous, radially fibrillose pileus, and clavate cystidia (Velenovský 1921). The original material does not exist, and the taxonomical value and position of *P. tiliaceus* remains unclear.

Pluteus praestabilis (Britzelm.) Sacc. was originally characterized by a blackish brown velvety pruinose pileus, a white stipe with brown floccules, basidiospores measuring $6 \times 4\text{--}5 \mu\text{m}$, and growth on soil near *Fagus sylvaticus* (Saccardo 1887: 672). Although it probably belongs to the *P. plautus* complex, *P. praestabilis* may also represent a species related to *P. podospileus* Sacc. & Cub. *Pluteus diana*e and *P. punctatus* have larger basidiospores, with *P. diana*e further distinguished by a stipe without brown floccules and a paler pileus.

Vellinga & Schreurs (1985) cited *Pluteus inflatus* Velen. as a synonym of *P. plautus*. However, our study of the holotype (PRM 154569!) showed that its pileipellis is composed of sphaeropedunculate and long elements, and pleurocystidia are absent. Our microscopical examination combined

with the macroscopic description by Velenovský (1921: 609) suggests that *P. inflatus* is closer to *P. podospileus* than to *P. plautus*.

The North American *Pluteus longistriatus* (Peck) Peck is characterized by a cinereous or whitish pileus, with striations that reach the darker, minutely squamulose-hairy disc, and a glabrous white stipe (Peck 1885). All these characters separate *P. longistriatus* from *P. diana*e and *P. punctatus*. Molecular data (FIG. 1) also support recognition of *P. longistriatus* as a separate taxon. Morphologically, *P. longistriatus* resembles the European *P. hiatus*ulus. Further phylogenetic and morphological research is needed to clarify the relationship between *P. longistriatus* and *P. hiatus*ulus.

As part of a project aiming to clarify the taxonomy of the North American *Pluteus* species, A. Justo revised the type collections of the 46 species described by Murrill (1911, 1917, 1939, 1943, 1946). Six belong to the *P. plautus* complex: *P. atriavellaneus* Murrill, *P. avellaneus* Murrill, *P. compressipes* Murrill, *P. fibrillosus* Murrill, *P. fuliginosus* Murrill, and *P. latifolius* Murrill. *Pluteus diana*e differs microscopically from them mainly by differently shaped pleurocystidia (only *P. latifolius* possesses pleurocystidia commonly bearing apical excrescences similar to *P. diana*e). *Pluteus punctatus* differs microscopically from the North American taxa mainly by its predominantly clavate to narrowly utriform cheilocystidia. *Pluteus latifolius* was originally described from Washington state, USA, growing on dead *Alnus* wood (Murrill 1917). Its pileus is avellaneous-isabelline, tomentose with a radiate-rugose centre, and ≤ 4 cm broad; the stipe is concolorous with the pileus and densely tomentose (Murrill 1917). *Pluteus latifolius* differs from *P. diana*e in its smaller basidiomata, smaller basidiospores ($5.2\text{--}7.2 \times 4.5\text{--}5.5$ μm , avg. = 6.2×4.8 μm , $Q = 1.18\text{--}1.39$, $\text{av}Q = 1.29$), and lageniform caulocystidia.

Pluteus atriavellaneus was described from Tennessee, USA, growing solitary on humus (Murrill 1917). In contrast to *P. diana*e, it is a small species (pileus ≤ 2 cm) with a dark fuliginous to avellaneous, hygrophaneous and finely pubescent pileus and white, smooth stipe (Murrill 1917). *Pluteus punctatus* differs from *P. atriavellaneus* by the presence of squamules on pileus and stipe.

Pluteus avellaneus was described from New York, USA, growing on unidentified dead wood (Murrill 1917). The pileus is described as small, hazel coloured, paler at centre, glabrous, hygrophaneous and ≤ 3.5 cm broad; the stipe is white and smooth (Murrill 1917). Its smaller pileus and stipe dimensions and hazel color of the smooth pileus distinguishes *P. avellaneus* from *P. diana*e. *Pluteus punctatus* differs from *P. avellaneus* by the presence

of squamules on pileus and stipe. Neither *P. punctatus* nor *P. diana*e have a hygrophanous pileus.

Pluteus compressipes is a tropical species from Jamaica, found growing on unidentified dead wood (Murrill 1917). Its pileus is rosy-isabelline with a darker centre, glabrous, and ≤ 4 cm broad and its stipe is white, smooth, and laterally compressed (Murrill 1917). Its occurrence in tropical areas and a smooth compressed stipe are significant differences from *Pluteus diana*e and *P. punctatus*.

Pluteus fibrillosus, collected in Louisiana, USA, from wet soil was characterized by a dark, innately fibrillose, ≤ 3 cm broad pileus and smooth white stipe (Murrill 1917). *Pluteus diana*e and *P. punctatus* differ by growth on decaying wood and a (sub)flocculose stipe. The pileus of *P. punctatus* is not innately fibrillose but floccose-squamulose, and the pileus of *P. diana*e is paler and larger.

Pluteus fuliginosus, from New York, USA and collected from a decayed *Pinus strobus* stump, was described with a uniformly coloured (fuliginous) pileus clothed with white hairs and ≤ 4 cm broad and a white to pale yellow or pale hazel and slightly squamulose stipe (Murrill 1917). The *P. fuliginosus* stipe was, as in *P. punctatus*, originally described as squamulose, although we observed no caulocystidia on the type collection. The cheilocystidia of *P. fuliginosus* are mostly lageniform or fusiform, and commonly provided with an apical excrescence (A. Justo, pers. obs.). Its habitat on conifer wood may be a reliable character to separate *P. fuliginosus* from other species in this complex, but additional collections are necessary to confirm this.

Conclusions

Our analyses confirm *Pluteus diana*e and *P. punctatus* as separate, molecularly supported species. We characterize *P. diana*e by rather large basidiomata, a whitish to greyish-brown pileus that may turn pale after drying, and a striate granulose-pruinose whitish stipe. Its striking microscopic features are its lageniform and fusiform pedicellate pleurocystidia with a narrowed apex often bearing a small apical excrescence, variable sized pileipellis elements, and caulocystidia in tufts.

Pluteus punctatus is characterized by medium sized basidiomata, a pale grey-brown pileus with ochraceous or (grey-) brown floccose squamules, and a whitish stipe with brown tomentose squamules. Microscopically striking are the rather short pleurocystidia, the long terminal elements in the pileipellis and caulocystidia that are isolated or occur in only small tufts.

Collections of *P. diana*e from central, eastern, and northern Europe show that this species is widespread in Europe. Moreover, it has also been documented from Turkey. The *P. punctatus* material of from Sweden is the only collection besides the holotype from Czechia. The distribution of both species should be further investigated.

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***Aecidium peristrophes*, a new record for Pakistan**

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ABSTRACT—During a survey of plant pathogenic fungi of Khanspur, Thandiani, and adjacent areas, two plant species—*Hedera helix* (Araliaceae) and *Peristrophe* sp. (Acanthaceae)—were found to be infected with rust fungi. After careful morphological and anatomical observations, these rusts were identified as *Aecidium hederæ* and *A. peristrophes*, with *A. peristrophes* reported as a new record for Pakistan.

KEY WORDS—Abbottabad district, aeciospores, *Pucciniales*

Introduction

Aecidium Pers. is an asexual genus of rust fungi that possesses non-repeating spores. Following dikaryotization of spermogonia, aeciospores are produced. Catenulate spores are the characteristic feature of this genus. These spores are surrounded by special structures called peridia (Cummins & Hiratsuka 2003). Although the asexual morph generic name is now considered a synonym of *Puccinia* and no longer recognized (Aime & al. 2018), a number of species previously described in this genus have not been placed in valid genera and thus must continue to be recognized in *Aecidium*. Seventeen species of this asexual morph genus are reported from Pakistan (Ahmad & al. 1997; Ishaq & al. 2018). During the 2016–18 surveys of pathogenic fungi, we collected plants of *Hedera helix* and *Peristrophe* infected with rust fungi. Based on their morphology these rusts were identified as *Aecidium hederæ* and *A. peristrophes*.

Materials & methods

Plants infected with rust fungi were collected from Khanspur and Thandiani forest, Khyber Pakhtunkhwa province, Pakistan. Healthy plants along with fruits



PLATE 1: *Aecidium peristrophes*, A. Infected host plant, *Peristrophe* sp., B. Infection under stereomicroscope, C. Aeciospores, D. Peridial cells. Scale bars: A = 5 mm, B = 1 mm, C, D = 10 μ m.

and inflorescence were also collected for identification. Host plants were identified by comparing with plants in the herbarium of Department of Botany, University of the Punjab, Lahore (LAH).

Scratch mounts and free hand sections of infected portions were made in lactophenol. Partial permanent slides were made by cementing glass cover slips with nail lacquer and slides were examined under a biological microscope (LABOMED,

Labo America, Inc. USA). Line drawings of different spore stages were made using a Camera Lucida (Ernst Leitz, Wetzlar, Germany). Dimensions of spores were taken using Scope Image 9.0(5X) with 40X objective. Forty spores were measured for each species.

Taxonomy

Aecidium peristrophes Syd. & P. Syd., Ann. Mycol. 10(3): 272 (1912) PLS 1–2

SPERMOGONIA, UREDINIA, and TELIA not found. AECIA epiphyllous, loosely arranged, yellowish brown, irregular. AECIOSPORES ovoid to angular, hyaline to subhyaline, 1–3 germ pores per cell, $16\text{--}23 \times 20\text{--}24\text{ }\mu\text{m}$; peridial cells hyaline to subhyaline, angular to hexagonal-pentagonal, $17\text{--}30 \times 19\text{--}28\text{ }\mu\text{m}$, wall verrucose, $2\text{--}5\text{ }\mu\text{m}$ thick.

MATERIAL EXAMINED: PAKISTAN, KHYBER PAKHTUNKHWA, Abbottabad District, Thandiani, at 2750 m asl, on *Peristrophe* sp. (*Acanthaceae*), 14 August 2018, N.S. Afshan, NSA#01 (LAH1408).

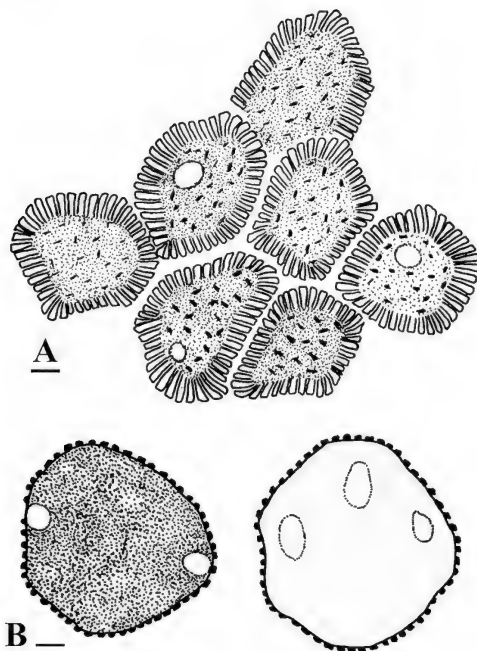


PLATE 2: Line drawings of *Aecidium peristrophes*,
A. Peridial cells, B. Aeciospores. Scale bars: A, B = 5 μm . (Drawings by Maria Riaz)

COMMENTS—*Aecidium peristrophes* was collected on *Peristrophe* sp. and represents a new record for Pakistan. It was previously reported on the same

host genus from China and India (Sydow & al. 1912, Laundon 1963, Zhuang 2001). *Puccinia peristrophes* Petr. was also reported on the same host plant from Malaysia (Petrak 1954), but aeciospores were not cited in the description. *Peristrophe* sp. is also reported here as a new host for rust fungi in Pakistan.

Aecidium hederæ Wakef., Bull. Misc. Inf., Kew 1931: 202 (1931)

PLS 3–4

SPERMOGONIA, UREDINIA and TELIA absent. AECIA amphigenous, cup-shaped, pale yellow to yellowish orange spots, mostly grouped, sometimes scattered, $1\text{--}3 \times 1\text{--}1.5$ mm. AECIOSPORES pale yellow to honey colored with yellowish orange granules, subglobose or ovoid–obovoid, $11\text{--}16 \times 15\text{--}23$ μm ; wall hyaline, verrucose, $1\text{--}3$ μm thick; peridial cells angular to subangular or rhomboidal, hyaline to pale yellow, $11\text{--}19 \times 15\text{--}26$ μm , wall verrucose to striolate verrucose, $2\text{--}4$ μm thick; germ pores obscure.

MATERIAL EXAMINED: PAKISTAN, KHYBER PAKHTUNKHWA, Abbottabad District, Khanspur, at 2250 m asl, on *Hedera helix* L. (Araliaceae), 3 May 2017, Najam ul Sehar Afshan NSA#02 (LAH1409); June 2018, N.S. Afshan, A.N. Khalid, NRP#02 (LAH14096).

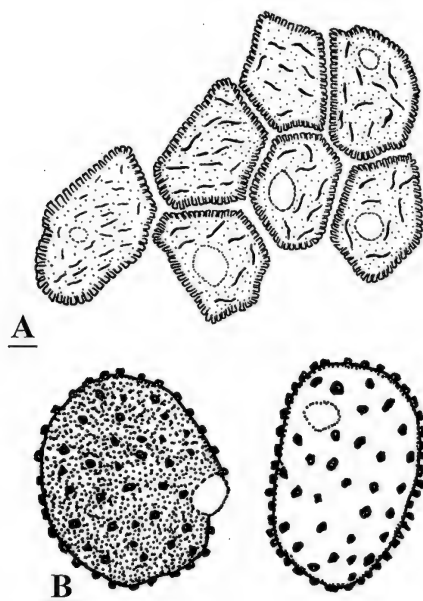


PLATE 3: Line drawings of *Aecidium hederæ*,

A. Peridial cells, B. Aeciospores. Scale bars: A, B = 5 μm . (Drawings by Maria Riaz)

COMMENTS—*Aecidium hederæ* has previously been reported from Pakistan on *Hedera helix* and *H. nepalensis* K. Koch from Murree and on *H. helix*

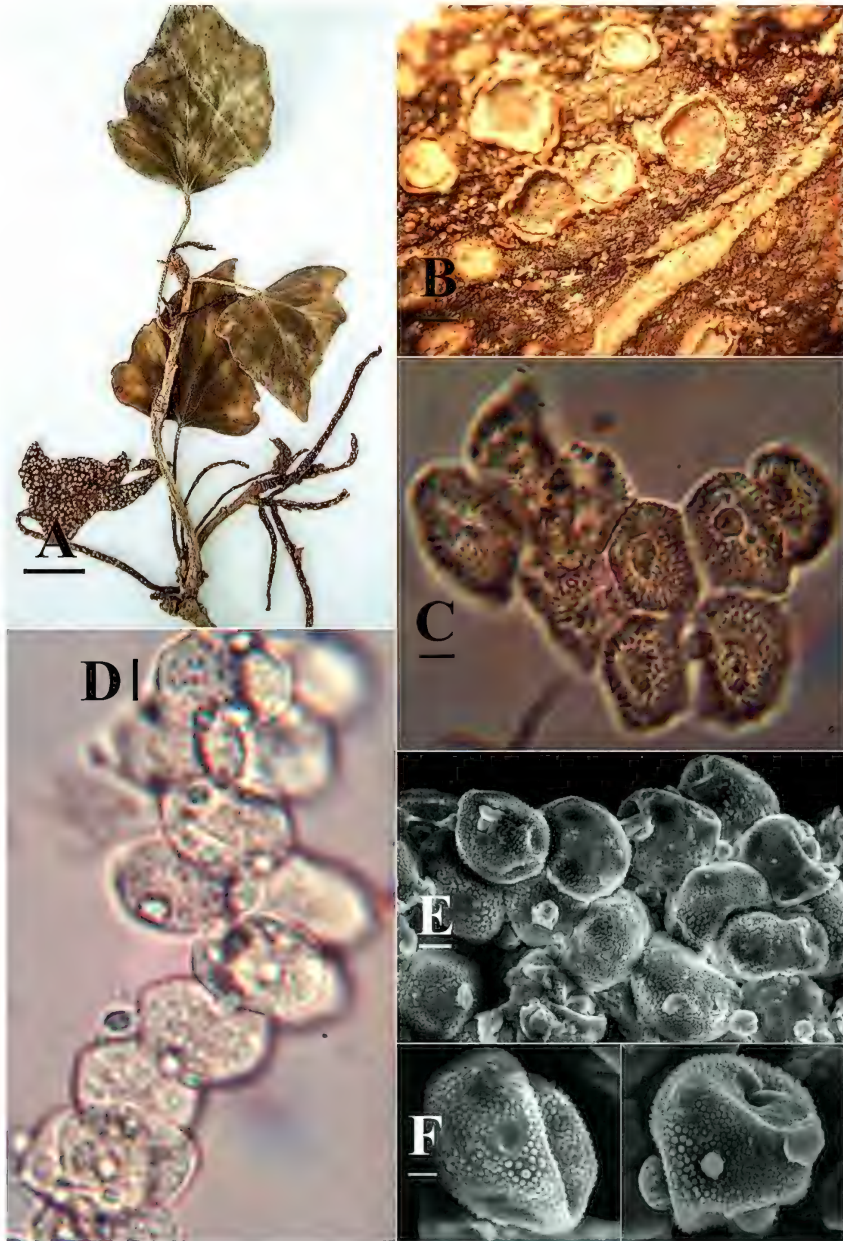


PLATE 4: *Aecidium hederae*, A. Infected host plant, *Hedera helix*; B. Detail of infection; C. Peridial cells; D. Aeciospores; E. SEM photograph of peridial cells; F. SEM photograph of aeciospores. Scale bars: A = 2 cm, B = 5 mm, C, D = 10 μ m, E, F = 5 μ m.

from Malkandi, Kaghan (Wakefield 1931, Ahmad 1956, Iqbal & Khalid 1996, Ahmad & al. 1997). The rust has also been reported on *Hedera himalaica* Tobler [= *H. nepalensis*] and *H. helix* from India (Farr & Rossman 2018). This is a new record for Khanspur, Pakistan.

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***Westerdykella aquatica* sp. nov., producing phytase**

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ABSTRACT—*Westerdykella aquatica*, isolated from rice field mud and as an endophyte from *Acorus calamus*, is described as a new species. The fungus is characterized by its globose cleistothecia, globose to subglobose, persistent, 8-spored asci, and cylindrical, 3-septate, light brown ascospores. A phylogenetic tree based on ITS, LSU, and β -tubulin sequences was constructed to infer the phylogenetic relationship between *W. aquatica* and other *Westerdykella* species in the genus. The new species was found to produce phytase, an important enzyme to release organic phosphorus in the soil.

KEY WORDS—Ascomycota, Dothideomycetes, freshwater fungi, phylogeny, Sporangiaceae

Introduction

Westerdykella Stolk was established to accommodate *W. ornata*, isolated from mangrove mud on the island of Inhaca, Mozambique, East Africa.

The genus is characterized by its globose, black and astomatous ascomata, membranous cleistothecium wall consisting of one layer of brown to black thick-walled cells, subglobose to elliptical multi-spored asci, and globose to subglobose, brown ascospores (Stolk 1955).

Currently, 13 additional species are accepted in *Westerdykella*: *W. angulata* (A.C. Das) Kruys, *W. aurantiaca* (J.N. Rai & J.P. Tewari) Kruys, *W. capitulum* (Panwar & al.) Gruyter & al., *W. centenaria* Crous & al., *W. cylindrica* (Malloch & Cain) Arx, *W. dispersa* (Clum) Cejp & Milko, *W. globosa* (J.N. Rai & J.P. Tewari) Tad. Ito & Nakagiri, *W. minutispora* (P.N. Mathur) Gruyter & al., *W. multisporea* (Cain) Cejp & Milko, *W. nigra* (Routien) Arx, *W. ornata* Stolk, *W. purpurea* (Cain) Arx, and *W. reniformis* Ebead & Overy (von Arx 1973, 1975, Cejp & Milko 1964, Crous & al. 2017, Ebead & al. 2012, Gruyter & al. 2013, Ito & Nakagiri 1995, Kruys & Wedin 2009, Stolk 1955).

Molecular phylogenies inferred from multi-loci showed that *Westerdykella* is monophyletic (Kruys & Wedin 2009; Ebead & al. 2012; Crous & al. 2017). However, morphologically some species do not fit well within the original generic concept (Stolk 1955). Therefore, a revision is needed to make the generic concept consistent with the species characters, and the asexual concept of the genus should be added.

Westerdykella species are an important bioresource, producing various bioactive substances such as antibiotics (Ebead & al. 2012; Xu & al. 2017b), cytotoxics (Xu & al. 2017a), enzyme inhibitors (Lee & al. 1997), and apoptosis inhibitors (Lee & al. 1999). During a long-term investigation of aquatic fungi (Hu & al. 2007, 2012a,b, 2017; Huang & al. 2018; Song & al. 2018a,b), a new *Westerdykella* species producing phytase was encountered in the mud of a rice field and also isolated as an endophyte of an *Acorus* plant in Jiangxi Province, China.

Phosphorus, an essential nutrient for the growth and development of living organisms, plays a vital role in virtually every plant process that involves energy transfer. Most organic phosphorus is in the form of phytic acid, an unavailable form of phosphorus. Phytase is an enzyme that releases the phosphorus from the phytate complex to make it available (Sandhya & al. 2015). The enzymatic degradation of phytic acid, which does not produce toxic by-products, is an environmentally friendly process (Ciofalo & al. 2003). In view of increasing demand, the production of phytase in a cost-effective manner using microorganisms is an important field of study (Shivanna & Venkateswaran 2014, Song & al. 2019). To the best of

our knowledge, this is the first paper assessing the phytase activities of the genus *Westerdykella*, a new bioresource of this enzyme.

Materials & methods

Sample collection and fungal isolation

Soil and plant samples were collected in various freshwater habitats in Jiangxi Province, China. The samples were placed in sterile ziplock plastic bags (Supin™) and brought back to the laboratory.

TABLE 1. Strains used in the phylogenetic analyses.

SPECIES	STRAIN NO.	GENBANK ACCESS. NO.		
		ITS	28S	β-tubulin
<i>Forliomyces uniseptatus</i>	MFLUCC 15-0765	KU721772	KU721762	—
<i>Preussia funiculata</i>	Huhndorf 2577	GQ203762	GQ203722	GQ203685
<i>P. typharum</i>	CBS 107.69	GQ203766	GQ203726	GQ203689
<i>P. vulgaris</i>	Strid 18884	GQ203767	GQ203727	GQ203690
<i>Sparticola juncei</i>	MFLU 16-0242	KY659562	KY659565	—
<i>Sporormia fimetaria</i>	Lundqvist 2302-c	GQ203768	GQ203728	GQ203691
	UPS: Dissing Gr.81.194	GQ203769	GQ203729	GQ203692
<i>Sporormiella irregularis</i>	Lundqvist 16568-f	GQ203780	GQ203739	GQ203700
<i>S. leporina</i>	MJR93/04	GQ203782	GQ203741	GQ203702
<i>S. vexans</i>	UME23	GQ203793	GQ203751	GQ203712
<i>Westerdykella angulata</i>	CBS 610.74	GQ203757	DQ384105	—
	IMI 090323	GQ203758	GQ203720	GQ203680
<i>W. aquatica</i>	JAUCC 1788 [T]	MH411093	MH411090	MH424907
	JAUCC 0138	MH411092	MH411091	MH424906
<i>W. aurantiaca</i>	FNBR-03	JN118571	—	—
	IMI 086825	AY943057	—	—
<i>W. centenaria</i>	CBS 142400	KY979734	KY979790	KY979908
	CBS 272.74	KY979735	—	—
<i>W. cylindrica</i>	ATCC 24077	AY943056	AY004343	Jx235707
<i>W. dispersa</i>	CBS 156.67	DQ468016	—	—
	CBS 297.56	GQ203797	GQ203753	GQ203716
	CBS 508.75	GQ203798	DQ384099	—
<i>W. globosa</i>	IFO 32588	AY943046	—	—
	SWC5	KY065369	—	—
	SWC6	KY260681	—	—
<i>W. minutispora</i>	CBS 509.91	-	GU238108	—
<i>W. multispora</i>	CBS 383.69	GQ203799	GQ203754	GQ203717
<i>W. nigra</i>	ATCC 12756	AY943049	—	—
	CBS 416.72	GQ203800	GQ203755	GQ203718
<i>W. ornata</i>	CBS 379.55	GQ203801	AY853401	GQ203719
<i>W. reniformis</i>	DAOM 242243	Jx235700	Jx235704	Jx235706
<i>Stemphylium vesicarium</i>	ATCC 11681	AF229479	AF382386	AY749032

Bold font indicates novel sequences generated in this study.

The soil samples were serially diluted up to 10^{-5} with sterile distilled water and spread on the surface of potato dextrose agar media (PDA) in plates, which were then incubated at 25 °C for 1–2 days. Stems of *Acorus calamus* were sliced into small lengths and cleaned 3–5 times with distilled water (Nonaka & al. 2013). Plant tissue pieces (c. 0.5 × 0.5 cm) were soaked in 75% alcohol for 30 seconds and immediately washed 3–5 times in sterile water, dried in a sterile fume hood for c. 5 minutes, and placed on PDA medium. Mycelium growing around the tissue was transferred to new PDA plates (Sati & al. 2009). Colonies with different morphological characters were transferred to new PDA plates. Cultures were dried as specimens and deposited in the Herbarium of Fungi, Jiangxi Agricultural University, Nanchang, China (HFJAU). Living cultures were deposited in the Culture Collection of Jiangxi Agricultural University, Nanchang, China (JAUCC).

Morphological studies

Strains were grown on PDA at 25 °C and their growth rates and colony morphology were evaluated after 7 and 14 days of incubation. The diameters of colonies were measured in five directions and the average values were applied to reflect the dimensions. For micro-morphological measurements and photographs, fungal structures from 30-day-old cultures were mounted in water on glass slides; and examined and photographed using a Nikon (Ni) compound microscope with differential interference contrast (DIC) and a dissecting microscope (Hu & al. 2017).

DNA extraction and PCR amplification

Genomic DNA of strains was extracted by CTAB (hexadecyl trimethyl ammonium bromide) method (Wu & al. 2001). Fragments of the partial large subunit (LSU), internal transcribed spacer (ITS) rDNA, and β -tubulin gene (Bt2) were amplified by the polymerase chain reaction (PCR). For PCR amplification, primer pairs LROR/LR6 were used for LSU (Rehner & Samuels 1995; Vilgalys & Hester 1990), ITS4/ITS5 for ITS (White & al. 1990), and T1/Bt2b for β -tubulin (Glass & Donaldson 1995, O'Donnell & Cigelnik 1997). The amplification was performed following the method described by Hu & al. (2012b). The PCR products were purified and sequenced with the same primers used for PCR in a sequencer (ABI-PRISM3730) at Tsingke Biological Technology Company, Beijing.

Phylogenetic analyses

Six novel sequences from the two strains of the new taxon (JAUCC 1788, JAUCC 0138) and reference sequences obtained from GenBank (TABLE 1), were aligned with MAFFT v.7 (<https://mafft.cbrc.jp/alignment/server/index.html>; Katoh & Standley 2013). The concatenated aligned dataset was analyzed separately using maximum likelihood (ML) and Bayesian inference (BI). The best-fit models of evolution for the three loci tested were estimated by MrModeltest V.2.2.

The ML analyses were conducted with RAXML v.7.2.6 (Stamatakis & Alachiotis 2010) using a GTRGAMMA substitution model with 1,000 bootstrap replicates. The robustness of the analyses was evaluated by bootstrap support (MLBS).

Posterior probabilities (PP) (Rannala & Yang 1996; Zhaxybayeva & Gogarten 2002) were determined by Markov chain Monte Carlo sampling (BMCMC) in MrBayes 3.0b4 (Huelsenbeck & Ronquist 2001). Six simultaneous Markov chains were run for 1,000,000 generations and trees were sampled every 100 generations (resulting 10,000 total trees). The first 25% of trees were removed as burn-in phase and the remaining trees were used to calculate posterior probabilities. Posterior probabilities values of the BI analyses (BPP) >0.95 were considered significant. Sequences generated in this study were deposited in GenBank (TABLE 1) and the final matrices and trees in TreeBASE (www.treebase.org; <http://purl.org/phylo/treebase/phyloids/study/TB2:S22878?x-access-code=7f62703b04d4f5d2876667f654bd0398&format=html>).

Phytase activity assessment

Mycelia obtained from fungal strains were inoculated to selective media (formula: calcium phytate 0.1%, dextrose 3.0%, NH_4NO_3 0.5%, KCl 0.05%, $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.05%, $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$ 0.003%, $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ 0.003%, agar 2%, pH 5.5) in a petri dish, and incubated in dark at 25 °C. Strains with transparent circles, indicating phytase activity, were selected for further phytase activity evaluation.

The selected fungi were inoculated in 50 mL volume of liquid medium (formula: dextrose 1.5%, peptone 0.3%, soluble starch 2%, $(\text{NH}_4)_2\text{SO}_4$ 0.2%, KCl 0.05%, $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.05%, $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$ 0.003%, $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ 0.003%, pH 5.5) in a 250 mL flask with two repeats. The fungi were fermented in a shaker at 28 °C, 160 rpm for 120 hours. The fermentation broth was sampled three times, each sample was centrifuged, and 10 mL of the supernatant were used to evaluate the phytase activity.

Phytase activity was evaluated by spectrophotometry according to the protocol of the Determination of Feed Phytase Activity (GB/T 18634-2009) provided by China National Standardization Administration (CNSA). One unit of phytase activity (U) was expressed as the amount of enzyme that liberates 1 μmol of inorganic phosphorus from a 5.0 mM sodium phytate solution per minute at 37 °C and pH 5.5, while enzyme production was expressed as phytase activity U/mL.

Results

Fungal strain isolation

Two fungal strains representing what proved to be a new species were obtained in this study. One strain JAUCC 1788 was isolated from rice field mud as a saprophyte, and another strain JAUCC 0138 was isolated from the stems of *Acorus calamus* as an endophyte.

Phylogenetic analyses

A multigene phylogeny, based on three loci, was used to infer the relationships between the new taxon and its allied species (FIG. 1). The resulting concatenated aligned dataset comprised 31 isolates representing six genera of

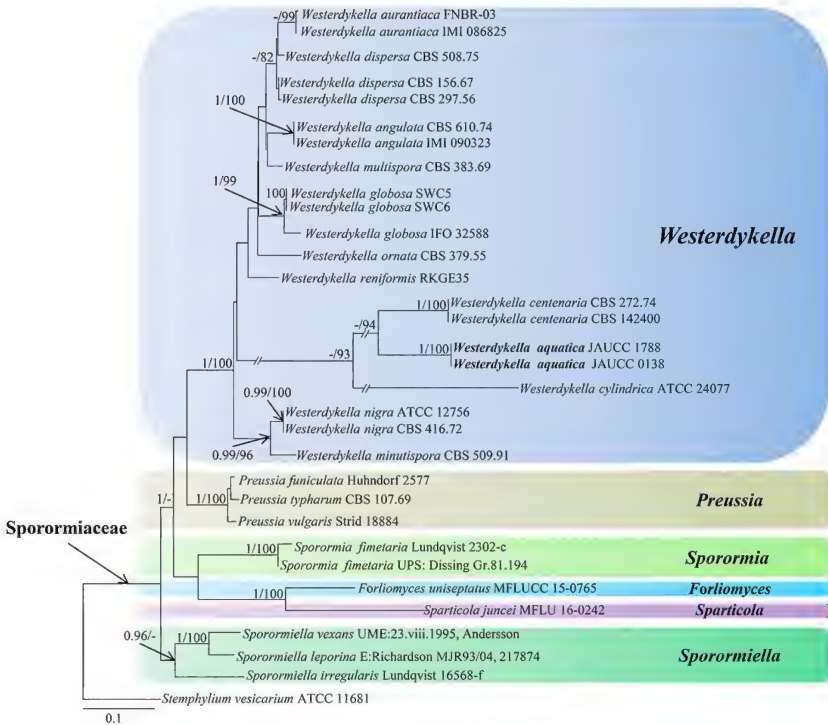


FIG. 1 Consensus tree inferred from a maximum likelihood analysis of ITS, LSU, and β -tubulin gene sequences. The RAxML bootstrap support values (MLBS) and Bayesian posterior probabilities (BPP) are given at the nodes (MLBS/BPP). The tree is rooted with *Stemphylium vesicarium* (ATCC 11681).

Sporormiaceae: *Forliomyces*, *Preussia*, *Sparticola*, *Sporormia*, *Sporormiella*, and *Westerdykella*; and an isolate of *Stemphylium vesicarium* (Wallr.) E.G. Simmons (*Pleosporaceae*) as outgroup. The dataset consisted of 1952 characters (448 for ITS, 815 for LSU, and 689 for β -tubulin, including alignment gaps). The trees generated from ML and Bayesian analyses of the individual loci (data not shown) and the combined dataset showed essentially congruent topologies. The ML tree based on the combined dataset is presented, with bootstrap support values (MLBS) and Bayesian posterior probabilities (BPP) indicated for well supported clades in FIG. 1. Two isolates of the new taxon (*Westerdykella aquatica*) together with other *Westerdykella* species formed a well-supported clade (BPP = 1, MLBS = 100%).

Phytase activity

The phytase activities of the two *Westerdykella aquatica* isolates are presented in TABLE 2.

TABLE 2. Phytase activity of *Westerdykella aquatica* strains.

STRAIN NO.	PHYTASE ACTIVITIES (U/mL)					
		Test 1	Test 2	Test 3	Average	Combined average
JAUCC 0138	Treat 1	0.079	0.114	0.096	0.096±0.014	0.085
	Treat 2	0.070	0.079	0.070	0.073±0.004	
JAUCC 1788	Treat 1	0.079	0.071	0.079	0.076±0.005	0.083
	Treat 2	0.079	0.176	0.018	0.091±0.065	

Taxonomy

Westerdykella aquatica H.Y. Song & D.M. Hu, sp. nov.

FIG. 2

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Differs from *Westerdykella angulata* and *W. purpurea* by its cylindrical and 3-septate ascospores; from *W. cylindrica* by its light brown ascospores; and from other *Westerdykella* species by its 8-spored asci.

TYPE—China, Jiangxi Province, Jingan County, isolated from mud in a rice field, 15 July 2017, Jun-Bo Zhang (Holotype, HFJAU 0676; ex-type living culture, JAUCC 1788; GenBank MH411090, MH411093, MH424907).

ETYMOLOGY—*aquatica*, referring to the aquatic habitat of the fungus.

COLONIES on PDA medium reaching 90 mm diam after 3 wk at 25 °C, spreading, flat, velvety, with sparse aerial mycelium, yellow, reverse dark yellow, slightly zonate, with several white rings, surface and margins smooth. Hyphae 1.4–4 µm diam, septate, branched, hyaline to light brown. SEXUAL STATE: Cleistothecia scattered, superficial, glabrous, globose, black, c. 100–260 µm diam. Peridium thin, membranous, composed of a single layer of globose to ellipsoidal, angular cells. Asci initials somewhat ovoid, later becoming globose to subglobose, 14–17 × 12–16 (mean = 15.3 × 14.1 µm, n = 30), persistent, 8-spored. Ascospores 17–38 × 2.5–4 µm (mean = 27 × 3 µm, n = 30), cylindrical, with rounded ends, 3-septate, slightly constricted at the septa, mostly separated into four segments at the very early stage of spore-formation in asci. Ascospore segments 4.5–11 × 2.5–3.5 µm (mean = 6.5 × 2.9 µm, n = 50), ellipsoidal, subhyaline, smooth-walled, light brown, mostly with a big guttule at each end, no germ-slits observed. ASEXUAL STATE: not observed.

ADDITIONAL SPECIMEN EXAMINED—CHINA, JIANGXI PROVINCE, Jiangxi Agricultural University, endophytic in *Acorus calamus* L. (*Acoraceae*) in a pond, 21 March 2014, Guan-Xiu Guan (HFJAU 0677; living culture, JAUCC 0138; GenBank MH411091, MH411092, MH424906).

Discussion

Westerdykella aquatica is characterized by its globose cleistothecia, globose to subglobose, persistent and 8-spored asci, and cylindrical, 3-septate, light brown ascospores. These characters fit well within the generic concept of *Westerdykella*. Furthermore, in the phylogenetic tree inferred from ITS, LSU, and β -tubulin genes, *W. aquatica* and other 19 reference strains of 11 species of *Westerdykella* form a well-supported clade (BPP = 1, MLBS = 100%).

Westerdykella aquatica resembles *W. angulata*, *W. cylindrica* and *W. purpurea* in having 8-spored asci. However, *W. aquatica* differs from *W. angulata* and *W. purpurea* in the shape of its ascospores. The ascospores of *W. aquatica* are cylindrical and 3-septate, while those of *W. angulata* and *W. purpurea* are angular (Das 1962; von Arx 1975; Kruys & Wedin 2009). *W. cylindrica* differs from *W. aquatica* in its reddish brown ascospores (Malloch & Cain 1972). Furthermore, the strains of *W. cylindrica* and *W. aquatica* are well separated in the phylogenetic tree (FIG. 1).

Although various chemical compounds have been reported from species of *Westerdykella* (Lee & al. 1997, 1999; Ebead & al. 2012; Xu & al. 2017a,b), our study is the first report of phytase production by the genus. Richardson (1994) reported that 20–80% of P in soils is found in the organic form, of which phytate (inositol hexaphosphate) is usually a major component. The benefits of phytase are its double effects on reducing the use of expensive inorganic phosphorus as fertilizer and its reduction of environmental pollution from excessive manure phosphorus runoff (Wang & Yang 2007). *Westerdykella aquatica* JAUCC 1788 was isolated from the mud of rice field, and its presence may help liberate P from the soil and reduce the use of P fertilizer.

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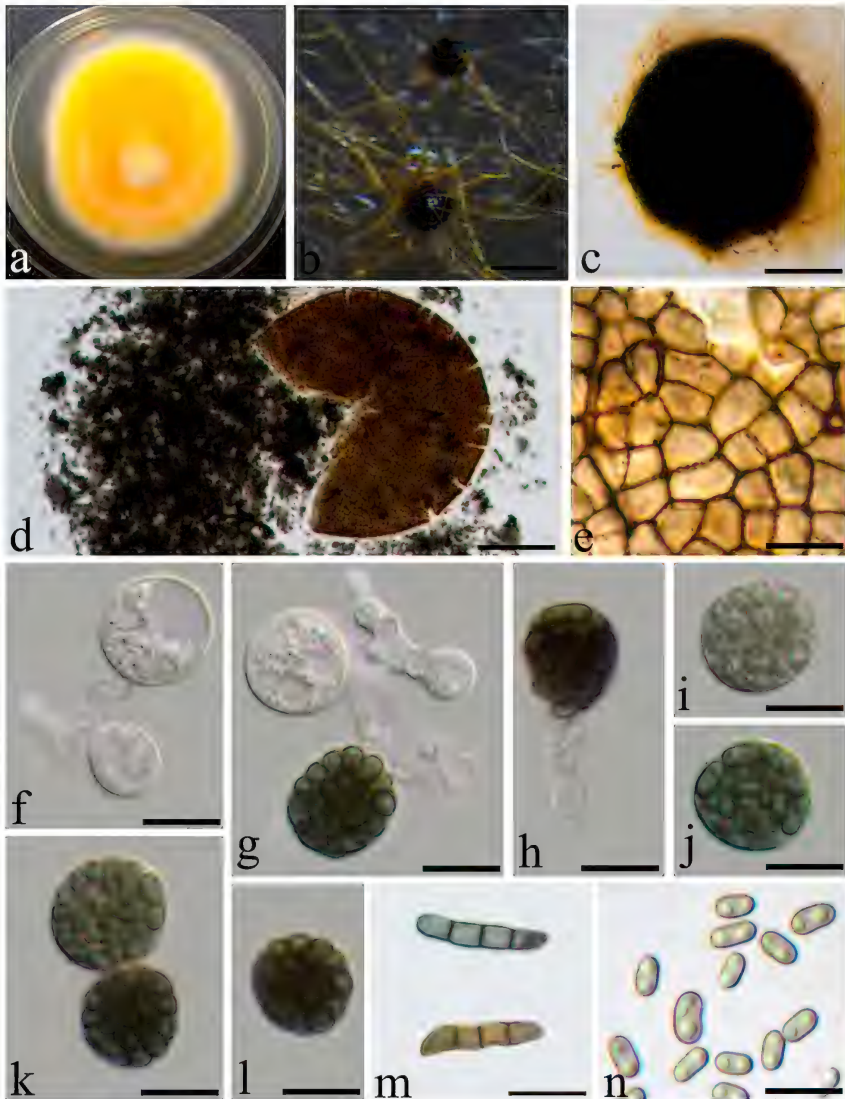


FIG. 2 *Westerdykella aquatica* (holotype, HFJAU 0676). a. Colony on PDA; b. Ascoma on PDA; c. Ascoma; d. Squashed ascoma; e. Peridium; f. Immature ascus; g-l. Asci; m. Ascospores; n. Ascospore segments. Scale bars: b = 1 mm; c, d = 100 µm; e-n = 10 µm.

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***Ramiphialis ronuroensis* gen. and sp. nov., a hyphomycete from the Amazonian rainforest**

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ABSTRACT—A new asexual ascomycete genus and species, *Ramiphialis ronuroensis*, was discovered on decaying leaves from Amazon rainforest in Brazil and is described and illustrated here. Morphologically, the fungus is distinguished by macronematous, monophialidic and multibranched, discrete, and terminal and intercalary conidiogenous cells that produce filiform to falcate, unicellular, hyaline conidia.

KEY WORDS—biodiversity, taxonomy, tropical fungi

Introduction

The discovery of new species is important to improve understanding of which and how many species will extinct (Costello & al. 2013). Although the Amazon occupies a prominent position in relation to global biodiversity, many species are disappearing due to the human actions. Studies on asexual fungi from Brazil have received more attention in Atlantic forest and Caatinga biomes (Barbosa & al. 2013, Fiuza & al. 2015, Santa-Izabel & Gusmão 2018). According to Sotão & al. (2004), little is known about asexual fungi in

Amazon. The northern region of the Amazon has more studies (Carmo & al. 2014, Castro & al. 2012, Hernandez-Gutierrez 2013, Monteiro & al. 2014) while in the southern region the investigations are still initial (Barbosa & al. 2015, 2017).

A survey of asexual ascomycetes on plant debris was carried out in the southern Amazon forest and an interesting fungus with branched conidiophores and phialidic conidiogenous cells is proposed here as a new genus and species.

Materials & methods

Samples of plant debris were collected in November 2016 at Rio Ronuro Ecological Station, Nova Ubiratã, Mato Grosso state (9°52'24"S 58°13'17"W) and placed in paper bags. In the laboratory, samples were washed and stored in moist chambers following Castañeda-Ruiz & al. (2016). After 72 h, the reproductive structures were mounted in PVL resin (polyvinyl alcohol, lactic acid, and phenol) and examined and photographed using a microscope equipped with phase contrast. Drawing was produced according Almeida & Gusmão (2015). The type specimen was deposited in the Herbario Centro-Norte Mato-Grossense, Sinop, Mato Grosso State, Brazil (CNMT).

Taxonomy

Ramiphialis F.R. Barbosa, Fiuza & R.F. Castañeda, **gen. nov.**

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Differs from *Atrosetaphiale* by its branched conidiophores, terminal phialides, and falcate conidia; from *Veramycina* by the absence of setae; and from *Jayarambhatia* by its conidiophores with extensions, discrete phialides, and falcate conidia.

TYPE SPECIES: *Ramiphialis ronuroensis* F.R. Barbosa & al.

ETYMOLOGY: Latin, *rami*, referring to the branched conidiophores; and *phialidis*, referring to the type of conidiogenous cells.

COLONIES scattered, dark brown. Mycelium superficial and immersed, composed of slightly branched, septate, smooth, brown hyphae. CONIDIOPHORES macronematous, mononematous, erect, straight or flexuous, branched, septate, with percurrent extensions, smooth, brown. CONIDIOGENOUS CELLS monophialidic, terminal and intercalary, discrete, determinate, pale brown. Conidial secession schizolytic. CONIDIA falcate, unicellular, hyaline accumulating in a white mucilaginous mass.

Ramiphialis ronuroensis F.R. Barbosa, Fiuza & R.F. Castañeda, **sp. nov.** Figs 1, 2

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Differs from *Atrosetaphiale flagelliformis* by its branched conidiophores, terminal phialides, and falcate conidia; from *Veramycina elegans* by the absence of setae; and from

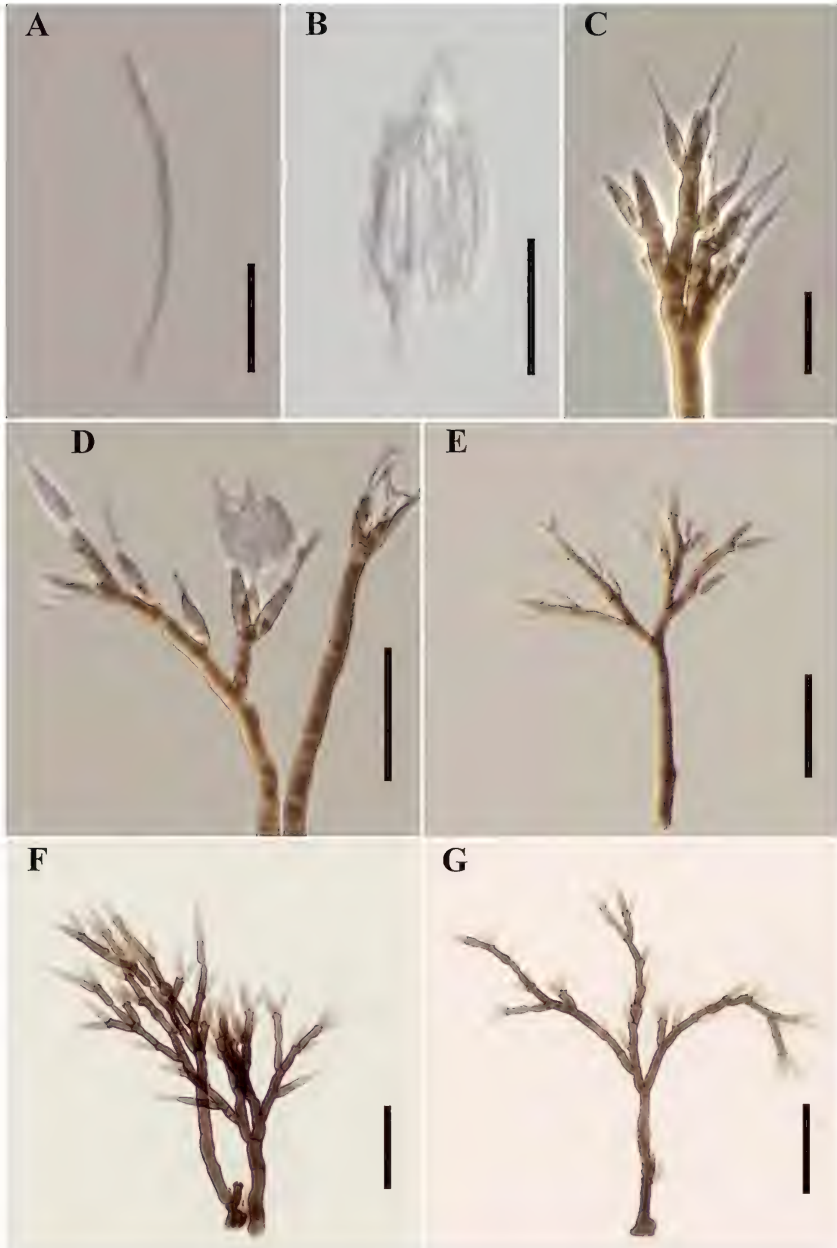


FIG. 1. *Ramiphialis ronuroensis* (holotype, CNMTf 80). A. Conidium; B. Conidia in mucilaginous mass; C, D. Conidiogenous cells and conidia; E–G. Conidiophores. Scale bars: A = 5 μm ; B = 10 μm ; C, D = 20 μm ; E = 40 μm ; F, G = 50 μm .

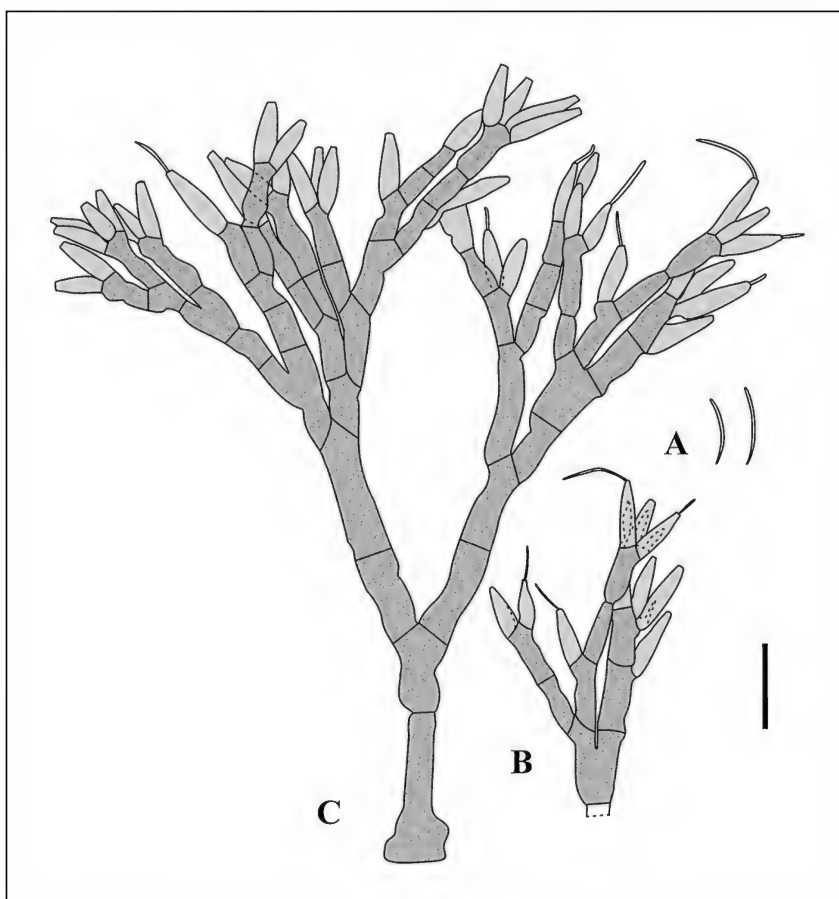


FIG. 2. *Ramiphialis ronuroensis* (holotype, CNMTf 80).

A. Conidia; B. Conidiophore, conidiogenous cells, and conidia; C. Conidiophore.

Scale bar = 20 μ m.

Jayarambhatia rhizophorae by its conidiophores with extensions, discrete phialides, and falcate conidia.

TYPE: Brazil, Mato Grosso State, Nova Uiratã, Estação Ecológica Rio Ronuro, on decaying leaves, 11.XX.2016, coll. F.R. Barbosa (**Holotype**, CNMTf 80).

ETYMOLOGY: Latin, *ronuroensis*, refers to the place where the species was collected.

COLONIES scattered, dark brown. Mycelium superficial and immersed, composed of slightly branched, septate, smooth, brown hyphae. **CONIDIOPHORES** macronematous, mononematous, erect, straight or flexuous,

multibranched, 5–12 septate, with percurrent extensions, smooth, brown, 130–200 × 6–9 µm. The branches are dichotomous starting near the lobed basal cell. CONIDIOGENOUS CELLS monophialidic, terminal and intercalary, discrete, sometimes forming subpenicillate clusters, evident, determinate, pale brown, cylindrical to slightly ovoid, 12.5–17.5 × 5 µm. Conidial secession schizolytic. CONIDIA filiform, falcate, hyaline, unicellular, smooth, 10–18(–25) × 0.5–0.7 µm, accumulating in a white mucilaginous mass.

COMMENTS—*Atrosetaphiale* Matsush., *Jayarambhatia* J. Pratibha, and *Veramycina* Subram. superficially resemble *Ramiphialis* in possessing phialidic conidiogenous cells that produce narrow conidia. *Atrosetaphiale*, however, is distinguished by its unbranched conidiophores and lateral and terminal phialides; its type species, *A. flagelliformis* Matsush., produces cylindrical-fusiform to flagellate conidia (Matsushima 1995), in contrast to the filiform conidia characterizing *R. ronuroensis*. *Jayarambhatia* differs in its determinate conidiophores, integrated phialides with elongated narrow necks, and narrowly obclavate conidia, while the generic type, *J. rhizophorae* J. Pratibha, produces much larger conidia (30–50 × 1 µm; Pratibha 2013). *Veramycina*, the synanamorph of *Oedemium* Link, is distinguished by the production of setae, conidiophores bearing terminal short branches, terminal and lateral phialides, and cylindrical to bacillar conidia; the generic type, *V. elegans* Subram., produces much shorter conidia (1.5–3 µm; Subramanian 1993). However, *Ramiphialis* does not produce setae and has dichotomously branched conidiophores.

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Phylogenetic placement of *Acrospeira*

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ABSTRACT —The morphology of *Acrospeira mirabilis* is described and illustrated based on a collection from Florida, USA. Phylogenies generated from ITS and LSU DNA sequence analyses place the genus *Acrospeira* in *Ceratostomataceae*. Based on molecular data, *Sphaerodes inferior* ($\equiv$ *Microthecium retisporum* var. *inferius*) is proposed as *Microthecium inferius* comb. nov.

KEY WORDS — asexual fungi, hyphomycete, synanamorph

Introduction

Acrospeira Berk. & Broome was erected and typified by *A. mirabilis* (Berkeley 1857, Berkeley & Broome 1861). Six out of eight species described in this genus have been transferred to other genera (Index Fungorum 2019, MycoBank 2019). With the seventh invalid because it lacks a Latin description (Art. 39.1, Shenzhen Code; Turland & al. 2018), *Acrospeira* has been reduced to its original monotypic status, containing only the type species, *A. mirabilis*. Its current phylogenetic and taxonomic placement is incertae sedis, *Pezizomycotina* (Index Fungorum 2019, MycoBank 2019, Wijayawardene & al. 2018).

A culture of *Acrospeira mirabilis* from a Florida 2018 collection allowed us to conduct a phylogenetic study using two loci (ITS and LSU) and determine its taxonomic placement using both morphological and molecular methods.

Materials & methods

Acrospeira mirabilis was obtained during a March 2018 collection trip in Largo, Florida. The fungus was plated on malt extract medium (MEA) (20 g malt, 20 g agar, 1 L distilled water), purified and subsequently grown at 25°C for 7 days for morphological observation and molecular work. The fungus was mounted in 85% lactic acid for microscopic observation and measurements with a Zeiss Imager. M2 compound microscope using differential interference contrast (DIC) and photographed with a Zeiss Axiocam 506 color camera. Fungal structures were measured using 40–100× objectives and statistically analyzed to determine standard deviations with 95% confidence interval of means.

The fungus culture has been deposited in the UAMH Centre for Global Microfungal Biodiversity at University of Toronto (UAMH), Canada.

DNA extraction, amplification, and sequencing

Genomic DNA was extracted from colonies grown in Petri plates according to the procedure in ZR Fungal/Bacterial DNA MicroPrep Kit. The oligonucleotides ITS5 and LR7 (Vilgalys and Hester 1990, White et al. 1990) were used to amplify a DNA fragment containing the internal transcribed spacer 1 and 2 region (ITS) and a portion of the large subunit rDNA region (LSU) by polymerase chain reaction (PCR) as described in Li & al. (2017). PCR products were purified using QIAquick PCR Purification columns; DNA concentration was determined on a ThermoScientific NanoDrop Lite Spectrophotometer. The purified PCR products were sequenced using oligonucleotides ITS2, ITS3 and ITS5, LROR, LR3R, LR3B, LR5 & LR7 (Vilgalys & Hester 1990, White & al. 1990, Li & al. 2017). The DNA was sequenced at the W.M. Keck Biotechnology Resource Laboratory, Yale School of Medicine (New Haven, CT, USA). New sequence information was deposited in GenBank (TABLE 1).

The ITS and LSU sequences were used in a BLASTn analysis of GenBank (<http://blast.ncbi.nlm.nih.gov>). To identify DNA sequences from allied taxa, BLASTn analysis was carried out with exclusion of uncultured/unidentified samples, environmental samples and samples with questionable identifications (Wheeler & al. 2003). Fungal DNA sequences linked to verified fungal voucher cultures that showed significant sequence similarity with the query sequences were chosen for phylogenetic analysis. Additional ITS and LSU sequences from allied taxa were obtained totaling 44 sequences from 32 fungi for phylogenetic analyses (TABLE 1).

Phylogenetic analysis

ITS and LSU sequences were aligned independently using MUSCLE (Edgar 2004) and manually corrected. The aligned sequences were trimmed and concatenated with FABOX sequence alignment joiner (http://users-birc.au.dk/palle/php/fabox/alignment_joiner.php).

TABLE 1. *Acrospira mirabilis* and taxa of allied genera and their sequences used in the phylogenetic analysis.

TAXON	COUNTRY	STRAIN #	ITS	LSU	REFERENCE
<i>Acrospira mirabilis</i>	USA	UAMH 12078	MN061697*	MN061697	This study
<i>Dactylidisporea ellipsospora</i>	Papua New Guinea	NBRC31376 T	LC146749	3137601	NBRC
<i>D. singaporensis</i>	Singapore	ATCC 38286 (NBRC 30865) T	LC146748	AY015629	Zhang & Blackwell 2002
<i>Gonatobotryum parasiticum</i>	Unknown	NBRC9010	901001	901001	NBRC
<i>Harzia acromonioides</i>	USA	NRRL 54328	HQ288051	HQ288051	D.T. Wicklow, ined.
	Unknown	NBRC 5937 (IMI 52642)	593701	593701	NBRC
	Unknown	NBRC 8881	888101	888101	NBRC
<i>H. cameroonensis</i>	USA	NRRL 54327	HQ698593	HQ698593	D.T. Wicklow, ined.
<i>H. macrospora</i>	Unknown	CBS 101.17	KY623402	KY623403	Schultes & al. 2017
<i>H. palmara</i>	France	CBS 101.42	KY623405	KY623406	Schultes & al. 2017
	Cameroon	CBS 136420 T	KF777163	KF777216	Crous & al. 2013
	Spain	CBS 122807	KY628683	KY628684	Schultes & al. 2017
	Unknown	NBRC8861	886101	886101	Schultes & al. 2017
	Indonesia	CBS 158.49	KY623396	KY623397	Schultes & al. 2017
	Turkey	CBS 995.69	KY623399	KY623400	Schultes & al. 2017
<i>H. patula</i>	Canada	CBS 121524	KY628686	KY628687	Schultes & al. 2017
	Canada	CBS 379.88	KY628689	KY628690	Schultes & al. 2017
<i>H. sphaerospora</i>	USA	UAMH 11865	KT221061	KT221062	Li & al. 2016
<i>H. tenella</i>	Romania	CBS 108.78	KY628693	KY628694	Schultes & al. 2017
	Former Yugoslavia	CBS 121.81	KY628696	KY628697	Schultes & al. 2017
<i>H. verrucosa</i>	Unknown	CBS 101.24	KY623414	KY623415	Schultes & al. 2017
	California	CBS 113456	KY628674	KY628675	Schultes & al. 2017
<i>Melanosporea damnosa</i>	France	CBS 113681 (NBRC 100318)	10031801	10031801	Marin-Felix & al. 2018

TAXON	COUNTRY	STRAIN #	ITS	LSU	REFERENCE
<i>Me. 'inaequalis'</i>	USA	NBRC 8426	842601	842601	NBRC
<i>Me. kursanoviana</i>	Russia	NBRC 8098	KP981479	809801	NBRC
<i>Me. mycoparasitica</i>	Canada	SMCD2220 T	F748922	F748916	Vujanovic & Goh 2009
<i>Me. pascuensis</i>	Chile	IMI 378527 T	AJ011312	—	Stchigel & al. 1999
<i>Me. tiffanyae</i>	Canada	SMCD2222	F748921	F748915	Vujanovic, ined.
<i>Me. verrucispora</i>	Papua New Guinea	NBRC 31375 T	KP981480	3137501	Martin-Felix & al. 2018
<i>Me. zambiae</i>	Israel	NBRC 32042	3204201	3204202	NBRC
	Unknown	NBRC 7902	790201	790201	NBRC
<i>Microthecium brevirostre</i>	Canada	ATCC 42427	—	AY015627	Zhang & Blackwell 2002
<i>M. ciliatum</i>	Japan	NBRC 9829 T	KP981481	KP981458	NBRC
<i>M. fimbriatum</i>	Unknown	NBRC 8615	861501	861501	NBRC
<i>M. fmicola</i>	Unknown	NBRC 8354	835401	835401	NBRC
	Japan	NBRC 9555	955501	955501	NBRC
<i>M. fusisporum</i>	Unknown	NBRC 8806	880601	880601	NBRC
<i>M. quadrangulare</i>	Spain	CBS 112763 T	KY628699	KY628700	Schultes & al. 2017
<i>M. tenuissimum</i>	Spain	CBS 112764 T	KY628705	KY628706	Schultes & al. 2017
<i>M. zobellii</i>	Unknown	NBRC 9442	944201	KP981476	NBRC
<i>Pseudomicrothecium subterraneum</i>	Unknown	BYTC Fan1001	—	JN247804	Fan & al. 2012
<i>Sphaerodes inferior</i>	Japan	NBRC 8366 T	836601	836601	NBRC
<i>Vittatispora coorgii</i>	India	BICC 7817 T	—	DQ017375	Rehner & Samuels 1995
<i>Xylaria hypoxylon</i>	USA	ATCC 42768	AY327477	U47841	Platas & al. 2004

ATCC = American Type Culture Collection, Manassas, United States; BICC = Biocoon culture collection, India; CBS = The Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; BYTC = Culture Collection of Capital Normal University, Beijing, China; IMI = IMI Fungarium, the Royal Botanic Gardens, Kew, UK; NBRC = the NITE Biological Resource Center, Japan; NFCCI = the National Fungal Culture Collection of India; NRRL = The Agricultural Research Service Culture Collection, USDA, USA; SMCD = the Saskatchewan Microbial Collection and Database, the University of Saskatchewan, Canada; UAMH = UAMH Centre for Global Microfungal Biodiversity, University of Toronto, Canada.

*The sequence accession numbers in bold indicate that these sequences were sequenced in this study.

The sequence dataset with 44 nucleotide sequences and 1039 positions was phylogenetically analysed using the maximum likelihood procedures, Tamura-Nei model, and uniform rates with MEGA7 (Kumar & al. 2016, Tamura 1992); all sites were treated equally. All sites were equally weighted, and gaps were treated as missing data. A bootstrap was calculated with 1000 replicates and posed statistical support at $\geq 70\%$. *Xylaria hypoxylon* ATCC42768 was designated as an outgroup.

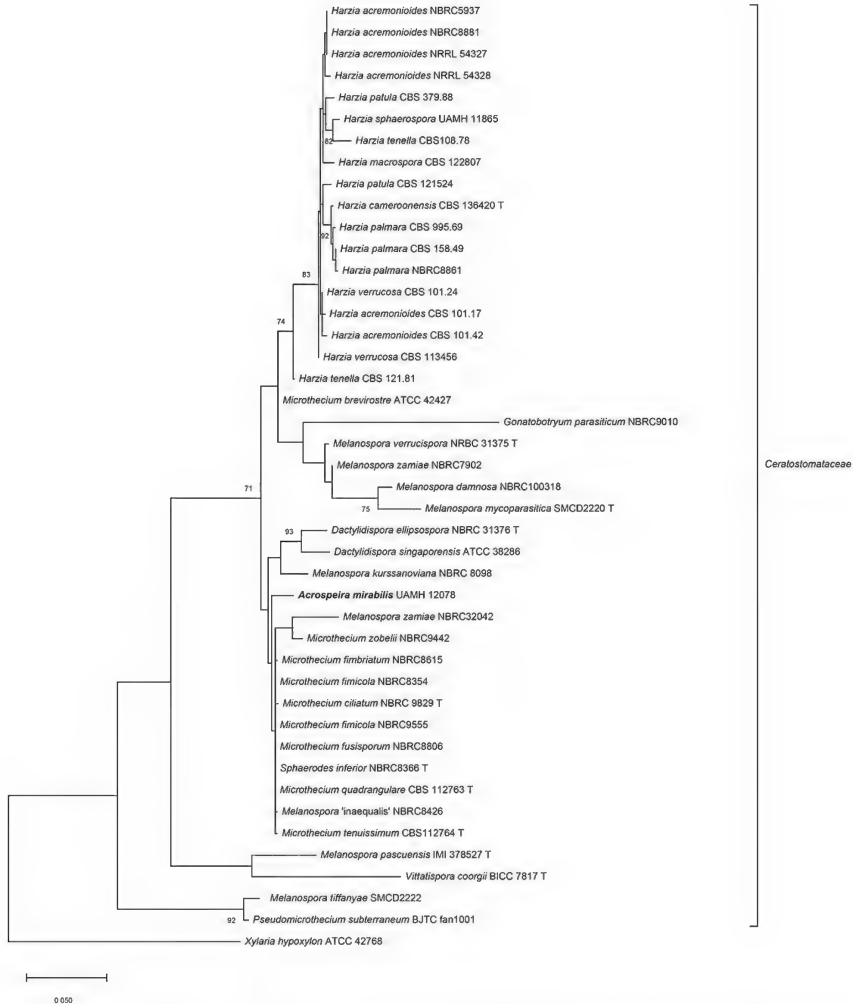


FIG. 1. Maximum Likelihood analysis of *Acrospeira mirabilis* and allied taxa, based on 44 sequences. *Xylaria hypoxylon* ATCC42768 is included as outgroup. The bootstrap test was conducted with 1000 replicates; bootstrap values $>70\%$ are indicated at the nodes. The scale bar indicates the number of expected changes per site. Annotations 'T' indicate the ex-type sequences included in the analysis.

Results

The ITS and LSU phylogenetic analyses place *Acrospeira mirabilis* in the same clade as genera in *Ceratostomataceae* (FIG. 1). *Acrospeira mirabilis* defines a sister clade to the clade including *Microthecium zobelii* (the generic type), *M. ciliatum*, *M. fimbriatum*, *M. fimicola*, *M. fusisporum*, *M. quadrangulare*, *M. tenuissimum*, *Sphaerodes inferior*, *Melanospora zamiae* NBRC32042, *Me. 'inaequalis'*, and *Me. zamiae* (NBRC32042) (FIG. 1).

Taxonomy

Acrospeira mirabilis Berk. & Broome, Intr. Crypt. Bot.: 305 (1857)

FIG. 2

This fungus is dimorphic. COLONIES attained 35 mm in 7 days on MEA at 25°C, cottony, chocolate brown. Mycelia immersed or aerial. Hyphae septate, hyaline, smooth, 3–6.8 µm diam.

DOMINANT STATE: CONIDIOPHORES semi-macronematous, mononematous, terminally or laterally arising from the hyphae and branched, hyaline, 15–35 µm long. CONIDIOGENOUS CELLS monoblastic integrated, terminal, determinate: branch ends enlarged and coiled, hyaline. CONIDIA solitary, dry, 3-celled, developed by dividing enlarged and coiled portion of conidiogenous cell with 2 transverse septa—the terminal cell enlarged greatly into a (sub)sphere, golden brown, tuberculate, (19.4–)21.9–27.1 (–30.5) µm diam. (mean ± SD = 24.5 ± 2.6 µm, n = 30), thick-walled; the median cell enlarged, smooth, hyaline to golden (paler than terminal cell), tuberculate, hemispherical, or dome-shaped, ornamented; and the basal cell hyaline to yellow and smooth—the whole conidia (23.7–)25.4–30.4 (–33.6) × (19.4–)21.9–27.1 (–30.5) µm (27.9 ± 2.5 × 24.5 ± 2.6 µm, n = 30), often with a visible germ pore on the enlarged (sub)spherical terminal cell. Conidial secession schizolytic.

SYNANAMORPH: phialidic conidial ontogeny. CONIDIOPHORES micronematous, mostly reduced to conidiogenous cells, arranged primarily on aerial hyphae, rarely on assimilative hyphae. CONIDIOGENOUS CELLS monophialidic, discrete, lageniform or ampulliform, rarely integrated, subulate, (5.5–)6.4–11.6 (–14.7) × (3.4–)3.6–4.4 (–4.9) µm (9.0 ± 2.6 × 4.0 ± 0.4 µm, n = 21), hyaline, smooth. CONIDIA basipetal, ellipsoid, ovoid, lacrimiform, subglobose or globose, 1-celled, hyaline, smooth, (2.4–)2.7–3.5 (–4.0) × (2–)2.2–2.8 (–3.1) µm (3.1 ± 0.4 × 2.5 ± 0.3 µm, n = 30).

SPECIMENS EXAMINED: UNITED STATES, FLORIDA: Largo, 27°53'02"N 82°48'31"W, on unknown leaf litter, 3.II.2018, coll. De-Wei Li (UAMH 12078).

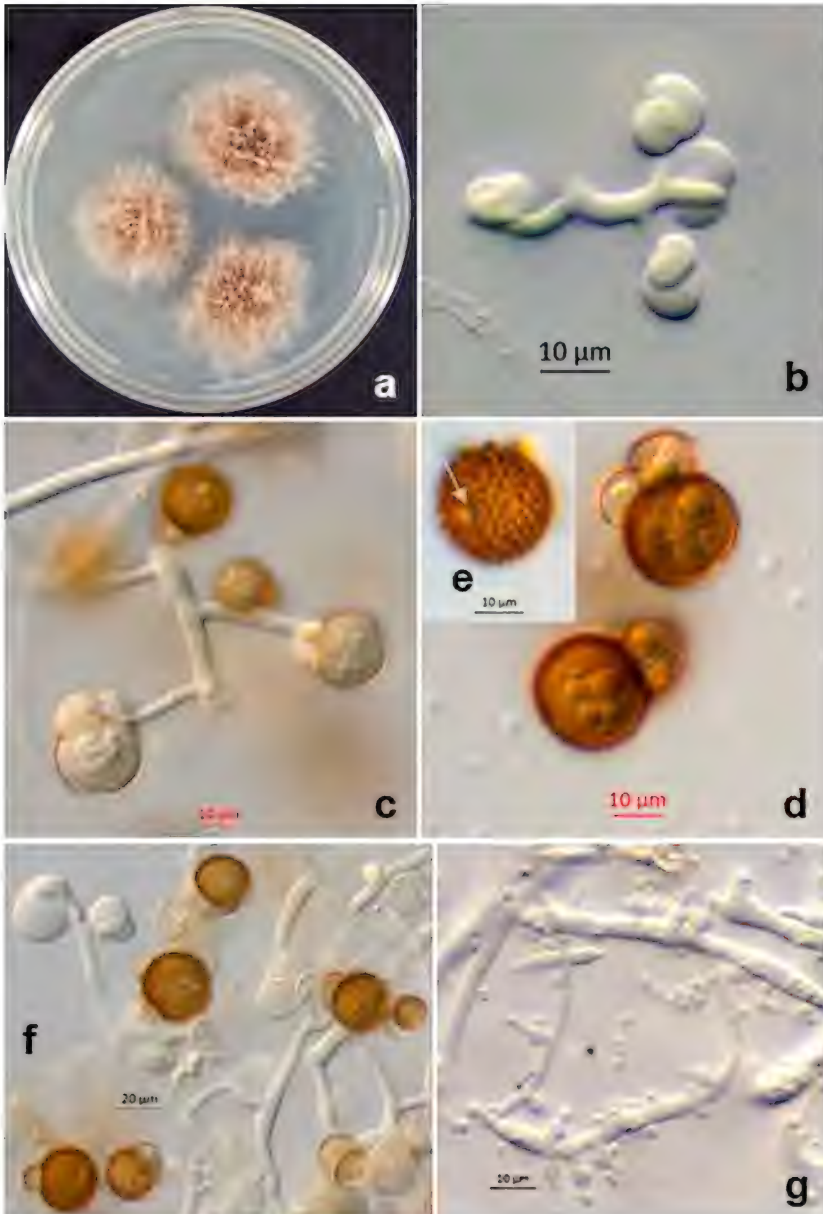


FIG. 2. *Acrospeira mirabilis* (UAMH 12078): a. colony grown on MEA for 7 days at 25°C; b. conidia at coiled stage and conidiophores; c. conidiophores, conidiogenous cells and conidia; d. conidia; e. surface ornament of conidium with a germ pore (arrowed); f. bimorphic states at different developmental stages; g. synnannamorphic state, conidia and phialides.

Discussion

Conidia of our collection are smaller than those of those described in previous reports (Berkeley 1857, Berkeley & Broome 1861, Ellis 1971). In USA, *A. mirabilis* has previously been reported from Florida, Massachusetts, and Michigan (Donis González & al. 2010, Farr & Rossman 2019).

Acrospeira has a phialidic synanamorph, while *Harzia* Costantin develops a proteophiala synanamorph. The proteophiala-like synanamorph is a key morphological character for merging the formerly accepted genera *Olpitrichum* G.F. Atk. and *Chlamydomyces* Bainier into *Harzia* (supported by phylogenetic analyses) and placing an emended *Harzia* in *Ceratostomataceae* (Li & al. 2016, Schultes & al. 2017). Whether the phialidic synanamorph plays a similar role in *Ceratostomataceae*, it is necessary to conduct further morphological and phylogenetic studies including other anamorphic and related genera. Seifert & al. (2011) suggested that *Acrospeira* belongs to *Ceratostomataceae*, but there is no phylogenetic study or discovery of the sexual state of the type species to support their statement. Our present phylogenetic results support the opinion of Seifert & al. (2011) and firmly demonstrate its taxonomic placement in *Ceratostomataceae*.

Microthecium was resurrected by Marin-Felix & al. (2018) for the M-S (*Melanospora-Sphaerodes*) 2 clade in Schultes & al. (2017). Marin-Felix & al. (2018), who examined the ex-type CBS 994.72 of *Sphaerodes retispora* var. *retispora*, suggested that it was contaminated by a host fungus and that *S. inferior* and *S. retispora* var. *retispora* were conspecific. They demoted *S. inferior* to a synonym of *S. retispora* based on their opinion that there were not enough morphological differences between the two species. However, although Marin-Felix & al. (2018) used the sequences of ex-type NBRC 8366 of *S. inferior* in their phylogenetic analysis, they did not include the sequences of ex-type *S. retispora* var. *retispora*. The sequence from the *S. retispora* ex-type fell into a clade with *Hypocrea schweinitzii* NBRC9063-T and *Trichoderma viridescens* CBS 433.34-T (Schultes & al. 2017), unrelated to *Fusarium* (the host fungus contaminant). We re-examined ex-type (CBS 994.72) of *S. retispora* var. *retispora*: the sexual stage did not develop on MEA, although the monophialidic anamorph was present. The culture was pure and we found no indication that the ex-type was contaminated. In our opinion, the relationship between *S. inferior* and *S. retispora* remains unsettled, and *S. inferior* should be retained as a separate taxon in *Microthecium*.

Microthecium inferius (Udagawa & Cain) D.W. Li, R.F. Castañeda & N.P. Schultes, **comb. nov.**

MB 831435

≡ *Microthecium retisporum* var. *inferius* Udagawa & Cain, Canad.

J. Bot. 47(12): 1928. 1970 ["1969"], as "*inferior*".

≡ *Sphaerodes retispora* var. *inferior* (Udagawa & Cain) P.F. Cannon & D. Hawksw., Bot. J. Linn. Soc. 84: 149. 1982.

≡ *Sphaerodes inferior* (Udagawa & Cain) D.W. Li & N.P. Schultes, Fung. Biol. 121(10): 901. 2017.

Our phylogeny places the unpublished *Melanospora* 'inaequalis' NBRC 8366 = TRTC 41540 in the *Microthecium* clade. The conserved strains of *Melanospora* 'inaequalis' need to be studied in the future. Further research of genera in *Ceratostomataceae* is also required, especially *Melanospora* s.l. and *Sphaerodes* s.l., given the polyphyletic characters of their representatives.

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***Golovinomyces asperifolii*: first record in China and *Bothriospermum chinense* as a new host**

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ABSTRACT—*Golovinomyces asperifolii* is described from the Qilian mountains in Qinghai province as a new record in China. The identification is supported by morphological characteristics and phylogenetic analysis of rDNA ITS. The fungus was collected on *Bothriospermum chinense*, which represents a new host for *G. asperifolii*.

KEY WORDS—Ascomycota, Boraginaceae, Erysiphaceae, powdery mildew, taxonomy

Introduction

The Qinghai-Tibet Plateau in China, known as “the ridge of the world,” has very special vegetation. *Bothriospermum chinense* is a Chinese endemic plant used as a traditional Chinese medicine for treating urinary tract infections. In autumn 2018, it was found to be heavily infected by a powdery mildew in the Qilian mountains, Qinghai. Based on the morphological characteristics of the asexual morph, the mildew was classified as a *Golovinomyces* sp. (Braun & Cook 2012). Molecular analyses were conducted to resolve the species identity. The internal transcribed spacer (ITS) regions were sequenced and compared with sequences in depositories. Based on sequence analysis of the rDNA ITS region, this species has been identified as *Golovinomyces asperifolii*.

This species has not previously been reported in China (Zheng & Yu 1987, Wu & Wu 1991, Chen 1993, Wang & al. 2002, Liu 2010, Bai 2015); our collection constitutes the first Chinese record of this species.

Materials & methods

Living leaves of *Bothriospermum chinense* bearing the anamorph of a powdery mildew were collected in autumn 2018 in the Qilian Mountains in China. The herbarium specimens were kept in Herbarium of Plant Pathology at Qinghai University, Xining, Qinghai Province, China (QHU).

A sample was mounted in distilled water and examined using an Olympus CX31RTSF light microscope. A JEOL JSM-6360LV scanning electron microscope was used to observe the anamorph ultrastructure, particularly conidial surface features (according to Cook & al. 1997) and hyphal appressoria.

Genomic DNA was extracted from the mycelium and the asexual morph using Chelex-100 (Walsh & al. 1991, Hirata & Takamatsu 1996). The nuclear rDNA ITS region (including the 5.8S gene) was amplified via polymerase chain reaction (PCR); PM5 and PM6 (Takamatsu & Kano 2001) were used to amplify the ITS region.

PCR assays were conducted in a 50 µL final volume (Hirata & Takamatsu 1996) containing 27 µL of 2× BoiStaq PCR MasterMix, 1 µL of each primer, 1 µL of the extracted DNA, and 20 µL of ddH₂O (Hirata & Takamatsu 1996). Thermal cycling in a BioRad PTC-200 thermal cycler comprised an initial denaturation step at 95°C for 5 min, 35 cycles at 94°C for 1 min + 60°C for 1 min + 72°C for 1 min, and a final elongation step at 72°C for 8 min. A negative control for each set of reactions replaced the template DNA with ddH₂O. The PCR products were separated by electrophoresis on a 2% agarose gel in TAE buffer and purified using the Zymoclean™ Gel DNA Recovery Kit, according to the manufacturer's instructions. The purified DNA products were ligated into the pMD18-T vector (Takara) and transformed into *E. coli* DH5α cells. The cloned fragments were sequenced by Sangon Biotech (Shanghai) Co., Ltd.

All DNA sequences were aligned using Clustal X 1.81 (Thompson & al. 1997), and the alignments were adjusted following Nei & Kumar (2000). All positions containing gaps or missing data were eliminated from the dataset. Cladistic trees were constructed using the neighbor-joining method with the Kimura 2-parameter substitution model in MEGA 4.0 (Tamura & al. 2007). Branch robustness was assessed by bootstrap analysis with 1000 replicates.

Taxonomy

Golovinomyces asperifolii(Erikss.) U. Braun & H.D. Shin,
Mycobiology 46(3): 198. 2018.

PLATE 1

Mycelium on leaves and stems, amphigenous, persistent, irregular white patches, thin, effuse; hyphae hyaline, smooth, 3–6 µm wide; hyphal appressoria nipple-shaped; conidiophores erect, 100–250 µm long; foot-cells

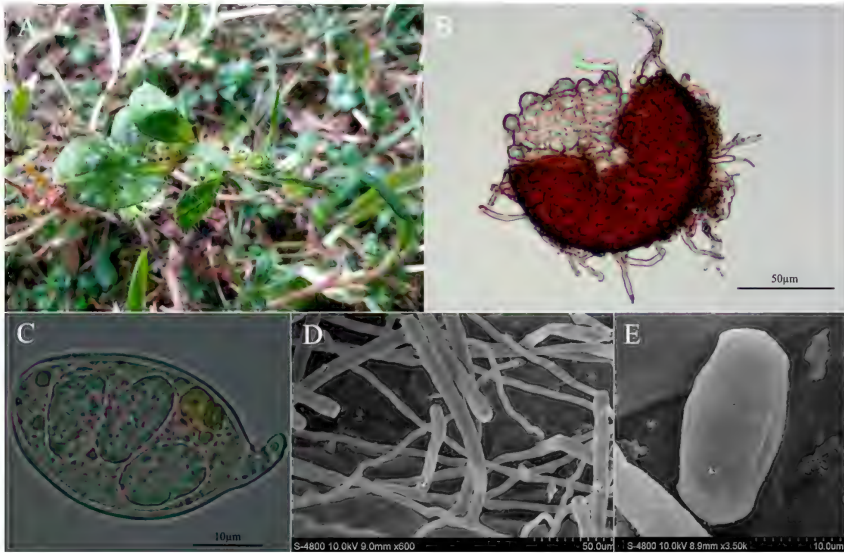


PLATE 1. *Golovinomyces asperifolii* (QHU2018043): A. *Bothriospermum chinense* infected by a powdery mildew; B. Chasmothecia and appendages; C. Ascus and ascospores; D. Conidiophore, conidia, and hyphae; E. Conidia.

straight, cylindrical, $40\text{--}130 \times 8\text{--}14\text{ }\mu\text{m}$, followed by 1–3 shorter cells; conidia ovoid to doliiform, with irregular longitudinal or reticulate ridges under the SEM, $22\text{--}38 \times 12\text{--}20\text{ }\mu\text{m}$, length/width ratio 1.4–2.4, Chasmothecia gregarious or sometime scattered, subglobose to globose, $80\text{--}110\text{ }\mu\text{m}$ diam; peridium cells irregularly polygonal, $8\text{--}23\text{ }\mu\text{m}$ diam; appendages more or less equatorial and in the lower half of the chasmothecia, numerous, mycelioid, simple, unbranched, interlaced with each other and with the mycelium, $0.4\text{--}2 \times$ times as long as the chasmothecial diam, $3\text{--}6\text{ }\mu\text{m}$ wide, septate, walls thin and smooth, hyaline or brown below and paler or colorless towards the tips; asci 6–12, with oil drops, ellipsoid-obovoid, clavate-saccate, $34\text{--}52 \times 20\text{--}31\text{ }\mu\text{m}$, short-stalked, 2–4-spored; ascospores ellipsoid-ovoid to almost globose, $10\text{--}19 \times 10\text{--}18\text{ }\mu\text{m}$, colorless.

SPECIMEN EXAMINED: , $38^{\circ}07'59''\text{N}$ $100^{\circ}08'38''\text{E}$, alt. 3280 m, on living leaves of *Bothriospermum chinense* Bunge (*Boraginaceae*), autumn 2018, L.C. Bai (QHU2018043; GenBank MK425651).

Phylogeny

The ITS rDNA sequence comprising 474 total characters was deposited in GenBank. The new sequence was aligned with sequences from eleven

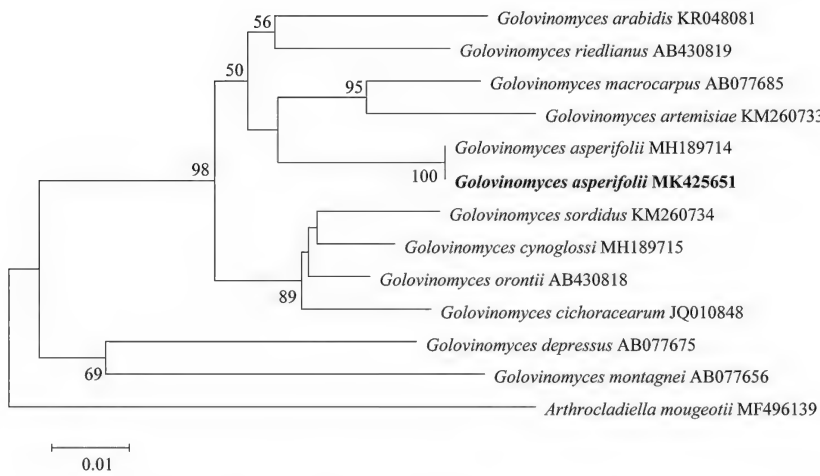


PLATE 2. A neighbor-joining tree based on distances derived from sequences of ITS1, ITS2, and the 5.8S rRNA gene from 12 *Golovinomyces* sequences and an *Arthrocladiella mougeotii* outgroup sequence. The bar indicates a distance of 0.01.

Golovinomyces spp. and an outgroup sequence of *Arthrocladiella mougeotii* (Lév.) Vassilkov (PLATE 2). The ITS phylogenetic tree placed the Chinese specimen and *Golovinomyces asperifolii* MH189714 (from Germany) in a strongly supported clade with 100% bootstrap support, indicating that these two sequences are conspecific.

Discussion

Golovinomyces asperifolii was described worldwide on hosts of the *Boraginaceae* in 2018. The chasmothecium we sampled agrees with the descriptions of *G. asperifolii* published by Braun & al. (2018), and its sequence was highly consistent with those reported. According to the host plant records for this powdery mildew (Braun & al. 2018), *Bothriospermum chinense* represents a new host for *G. asperifolii*.

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***Cercospora* *bundelkhandae* comb. nov. from India**

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ABSTRACT—The new combination *Cercospora bundelkhandae* (= *Pseudocercospora bundelkhandae*) is proposed, based on critical morphological re-examination of the holotype specimen and fresh topotypic material and comparison with closely related species of cercosporoid hyphomycetes. The species was originally collected on living leaves of *Tinospora sinensis* from Jhansi, Utttar Pradesh, India.

KEY WORDS—anamorph, *Capnodiales*, *Mycosphaerellaceae*, nomenclature, taxonomy

Introduction

The hyphomycetous ramularioid complex (*Mycosphaerellaceae*, *Capnodiales*) comprises genera with colourless conidiophores and conidia. The morphologically most similar genera of this complex are *Cercospora* Sacc., *Pseudocercospora* Deighton, and *Ramularia* Unger. The taxonomic problems presented by this complex were discussed by Braun (1990, 1991a,b, 1994, 1995, 1998), Kirschner (2009), Crous & al. (2001a,b), Verkley & al. (2004), and Videira & al. (2016). In *Cercospora* the conidial scars and hilum are thickened while in *Ramularia* they are only slightly thickened. These criteria however are somewhat subjective and, in many descriptions, become merged or modified as ‘slightly thickened and darkened’ or

'refractive.' These difficulties explain the frequent transfers of *Cercospora* species to *Ramularia* and vice versa. Scanning electron microscopy has shown that conidiogenous loci are smooth (a flat conidiogenous locus shaped as a truncated cone) in *Cercospora* but resemble *Cladosporium*-type loci (consisting of a circular rim and a central dome) in *Ramularia* (Kirschner 2009, Bensch & al. 2012). Braun (1995) separated *Cercospora* into two subgenera—*C. subg. Cercospora* and *C. subg. Pseudovellosiella* U. Braun—based on the presence or absence of secondary superficial mycelium and development of conidiophores from stromata or secondary superficial mycelia or both. *Cercospora* are primarily hyaline, although in tropical and subtropical countries, some *Cercospora* species occur with olivaceous or pale olivaceous-brown stromata and coloured conidiophore bases (Braun 1995).

A large number of ramularioid fungi have been recombined in the genus *Cercospora* from all over the world (Braun 1992, 1993; Davis 1919, 1924; Deighton 1973; Höhnelt 1924; Magnus 1906; Saccardo 1895). Recently, additional ramularioid species have been described from India (Awasthi & al. 2016, Singh & al. 2008), suggesting that the diversity of such fungi is still insufficiently known in this region.

During a survey of the Jhansi region of Uttar Pradesh in 2018, a colourless foliicolous hyphomycete found on leaves of *Tinospora sinensis*, was identified as species of *Cercospora* subg. *Cercospora* due to presence of prominent thickened conidial scars and hilum. A literature survey revealed that this fungus had been described earlier as *Pseudocercospora bundelkhandae* (Shrivastava & al. 2009). As the fungus is characterized by thickened scars and colourless conidiophores and conidia and the absence of secondary superficial mycelium and solitary conidiophores, it is taxonomically worthwhile to transfer the species into *Cercospora* subg. *Cercospora*.

Materials & methods

The holotype specimen [conserved in the Herbarium, Division of Mycology & Plant Pathology, Indian Agricultural Research Institute, New Delhi, India (HCIO)] and a fresh specimen collected from living *T. sinensis* leaves from the type locality [conserved in the Mycological Herbarium, Banaras Hindu University, Varanasi, India (MH-BHU)] were examined in lacto-glycerol-cotton blue using an Olympus Magnus CH20i-TR light microscope. At least 50 measurements of each fungal structure were taken for taxonomic diagnoses. Histological sections were prepared in order to observe the relationship between the fungus and the host tissue. The fungus was compared with closely related cercosporoid taxa by the help of current literature.

Taxonomy

Cercospora bundelkhandae (S. Shrivast., N. Verma & A.N. Rai) Raghv. Singh,
S.K. Verma, S. Yadav & Sh. Kumar, **comb. nov.** FIG. 1

MB 831083

≡ *Pseudocercospora bundelkhandae* S. Shrivast., N. Verma &
A.N. Rai, J. Mycol. Pl. Pathol. 39(2): 305 (2009)

(Description based on type material): INFECTION SPOTS amphigenous, circular to irregular, 3–10 mm in diam., initially hyaline, then becoming very light- to mid-brown. COLONIES amphigenous, effuse. Mycelium internal. STROMATA well developed, immersed, pseudo-parenchymatous, hyaline to olivaceous or light olivaceous-brown, 35–50 µm in diam. CONIDIOPHORES macronematous, 5–10 fasciculate, sometimes synnematous, unbranched, erect to procumbent, straight to flexuous, geniculate, smooth, 2–5-septate, thick-walled, hyaline, (18–)50–80(–85) × 2.5–5(–7) µm. CONIDIOGENOUS CELLS integrated, terminal, polyblastic, sympodial, mostly conspicuously geniculate, cylindrical, usually swollen at apex; loci thickened, darkened, outwardly bulging, 2–3.5 µm wide. CONIDIA simple, solitary, acropleurogenous, obclavate-cylindrical, ellipsoid, straight to slightly curved, apex subacute, base subconic-truncate, dry, smooth, thin walled, 1–4-septate, hyaline, (10–)20–55(–65) × (2–)3–6(–8.5) µm, hilum thickened, 2–3.5 µm wide.

SPECIMEN EXAMINED: INDIA, UTTAR PRADESH, Jhansi, on leaves of *Tinospora cordifolia* (Willd.) Miers [= *T. sinensis* (Lour.) Merr. (*Menispermaceae*)], 10 December 2010, leg. S. Jain (HCIO 44091, holotype); Jhansi, 25.4484°N 78.5685°E, on living leaves of *Tinospora sinensis*, December 2018, leg. Raghvendra Singh (MH-BHU 9).

Discussion

Cercosporoid fungi previously reported on *Tinospora* hosts include: *Cercospora madhauensis* Kamal & al.; *Cercospora dioscoreophylli* (Henn.) Deighton; *Passalora menispermi* (Ellis & Holw.) U. Braun & Crous; *Pseudocercospora cocculi* (Syd.) Deighton; *Ps. tinosporae* A.N. Rai & Kamal; *Ps. tinosporicola* U. Braun & Bagyan.; and *Ps. tinosporigena* U. Braun (Deighton 1973, 1976; Braun & Crous 2005; Crous & Braun 2003; Bagyanarayana & Braun 1992; Rai & Kamal 1989; Kamal & al. 1987).

Molecular sequence data have already confirmed that the presence/absence of thickened and darkened conidiogenous loci, slightly thickened and darkened or refractive scars (refractivity indicating the absence of scar), presence/absence of conidiophore and conidial pigmentation, and planate/pileate thickened dark conidiogenous loci are taxonomically important

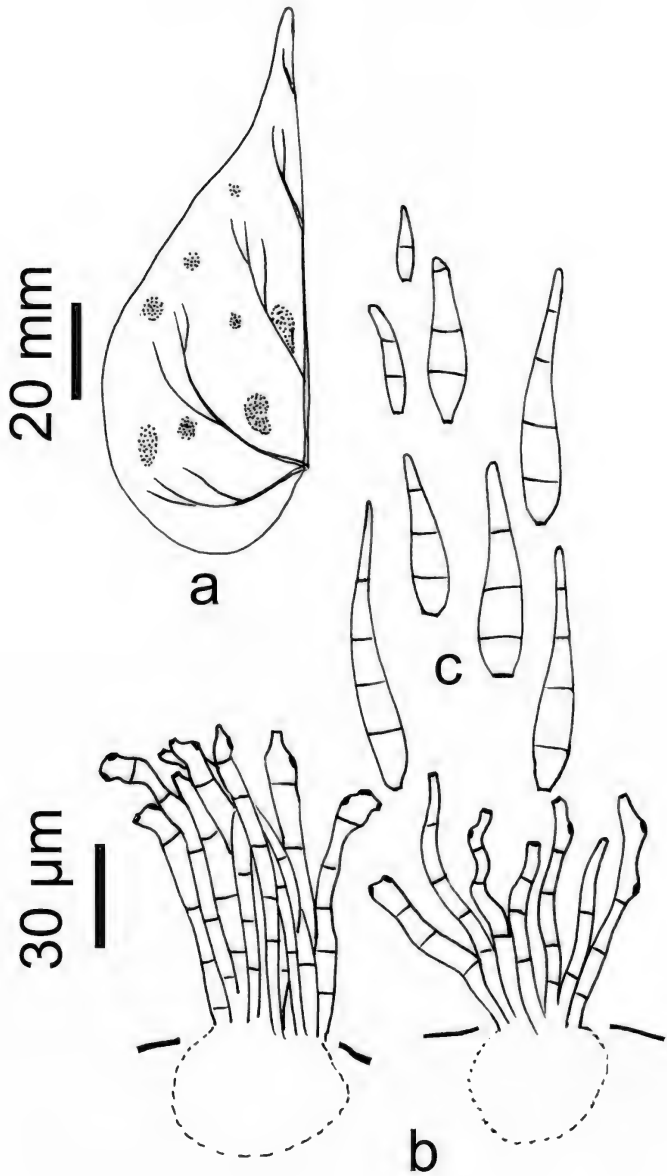


FIG. 1. *Cercospora bundelkhandae* (holotype, HCIO 44091):
a. Symptoms; b. Stromata with fascicle of conidiophores and conidiogenous cells; c. Conidia.

features (Crous 1999; Untereiner 2000; Crous & al. 2000, 2001a,b; Pretorius & al. 2003; Stewart & al. 1999; Taylor & al. 2003).

Cercosporella bundelkhandae differs from *Cercospora madhauensis*, *P. menispermi*, *Ps. cocculi*, *Ps. tinosporae*, *Ps. tinosporicola*, and *Ps. tinosporigena* because they all have either coloured conidiophores or coloured conidia or both.

Due to its hyaline nature, *Cercosporella bundelkhandae* shows a close resemblance to *C. dioscoreophylli*, distinguished by its longer ($180 \times 3\text{--}5.5\ \mu\text{m}$) branched conidiophores and longer, pluriseptate conidia ($25\text{--}80 \times 3\text{--}7.5\ \mu\text{m}$, 1–6-septate).

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***Coprinellus ovatus* sp. nov. from Pakistan**

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ABSTRACT—A *Coprinellus* specimen collected in Islamabad, Pakistan, showed characters that were distinct from those of all other *Coprinellus* spp.: an ovoid shaped pileus; a caespitose stipe base; utriform cheilocystidia bearing crystals; a pileipellis of loosely arranged clavate to mucronate hyphae; and basidiospores ($9.5\text{--}11.6 \times 6.0\text{--}7.8 \times 5.6\text{--}6.2\ \mu\text{m}$) with shapes ranging from mitriform or triangular to ellipsoid in face view, amygdaliform to ellipsoid in side view. Combination of all these characters and molecular analysis of ITS sequences support its identification as a new species.

KEY WORDS—coprinoid mushrooms, *Micacei*, *Psathyrellaceae*, taxonomy

Introduction

Coprinoid mushrooms are an important group of macrofungi that can be readily distinguished from normal agarics by having gills that liquify at maturity. As a result, coprinoid mushrooms are often called inky caps. Coprinoid mushrooms, which are characterized by thin fragile pilei that become plicate on opening, deliquescent gills, and dark brown to blackish basidiospores with germ-pores (Schafer 2014), spread across *Agaricales* in evolutionary lineages that are either fully or partially coprinoid (Tóth & al. 2013). Fully coprinoid genera include: *Coprinus* Pers., *Coprinellus* P. Karst., *Coprinopsis* P. Karst., and *Parasola* Redhead & al. Some species of *Leucocoprinus* Pat., *Conocybe* Fayod, *Bolbitius* Fr., and *Galerella* Earle show coprinoid combinations of characters (Matheny & al. 2006, Nagy 2011, Nagy & al. 2011, Tóth & al. 2013).

Coprinellus, with approximately 84 described species, represents an independent lineage in *Psathyrellaceae* (Redhead & al. 2001; Walther & al. 2005; Padamsee & al. 2008; Vašutová & al. 2008; Nagy & al. 2011, 2012, 2013; Örstadius & al. 2015; Hussain & al. 2018a). These mushrooms are commonly found on bare soil, wood chips, grassy debris, leaf-litter, and herbivore dung (Schafer 2010). *Coprinellus* species are divided into three sections based on veil anatomy and the presence or absence of cap pileocystidia. *Coprinellus* sect. *Domestici* (Singer) D.J. Schaf. is characterized by a pileus veil comprising floccose scales consisting of chains of fusiform or subglobose cells, often with encrusted walls. In *C. sect. Micacei* (Fr.) D.J. Schaf., veil remnants are present in the form of scattered (often disappearing) granulose flocks of globose cells arising from a matrix of narrow branched hyphae. In *C. sect. Setulosi* (J.E. Lange) D.J. Schaf., the veil may be present or absent, but the pileus and stipe are covered with thin-walled pileocystidia and caulocystidia, respectively (Schafer 2010). However, Nagy & al. (2012) showed that molecular phylogeny did not entirely support these sections in that clades corresponding to *C. sect. Micacei* and *C. sect. Domestici* each included some setulose species.

Twenty-two coprinoid species have been reported from Pakistan (Ahmad & al. 1997; Hussain & al. 2016, 2017, 2018a,b), of which eight belong to *Coprinellus*: *C. campanulatus* S. Hussain & H. Ahmad, *C. disseminatus* (Pers.) J.E. Lange, *C. disseminatisimilis* S. Hussain, *C. marculentus* (Britzelm.) Redhead & al., *C. micaceus* (Bull.) Vilgalys & al., *C. pakistanicus* Usman & Khalid, *C. radians* (Desm.) Vilgalys & al. *C. tenuis* S. Hussain (Ahmad & al. 1997; Hussain & al. 2018b).

During surveys of basidiomycetous fungi of Pakistan in 2018, one interesting collection presenting a *Coprinellus* morphology was encountered. Closer inspection revealed that this collection presented a unique combination of features compared with other *Coprinellus* species. Here we propose a new species based on morphological characters and molecular phylogenetic analysis of rDNA internal transcribed spacer (ITS).

Materials & methods

The sample was collected from the capital territory Islamabad, Pakistan, along the Murree Express Road. Islamabad (33.43°N 73.04°E) lies at the edge of the Pothohar Plateau at the base of the Margalla Hills, occupies an area of 906 km² with elevation of 507 m a.s.l., and has a humid subtropical climate (Köppen climate classification). The territory recognizes winter (November–February), spring (March–April), summer (May–June), rainy monsoon (July–August), and autumn (September–October), with June the hottest month with the average temperature routinely exceeding 38°C

TABLE 1. *Coprinellus* and *Psathyrella* species and specimens used for the molecular phylogenetic analysis.

SPECIES	VOUCHER	COUNTRY	ITS #
<i>C. aff. eurysporus</i> (as <i>C. sp.</i> in GenBank)	NL-3418	Hungary	JN159540
<i>C. aff. xanthothrix</i> (as <i>C. xanthothrix</i> in GenBank)	NL-1292	Sweden	FM878008
<i>C. angulatus</i>	NL-1934	Hungary	HQ846994
	Arnolds99-22	Netherlands	JN159536
	NL-0906	Hungary	JN159535
<i>C. bisporiger</i>	WU7403	Hungary	HQ846974
	Daams71-98	Hungary	JN159520
<i>C. bisporus</i>	NL-0158	Sweden	GU227705
	NL-2512	Sweden	FN396107
	WU6011	Sweden	JN159517
<i>C. brevisetulosus</i>	NL-1445	Hungary	GU227710
<i>C. callinus</i>	NL-1931	Hungary	FN396105
	Ulje1204	Netherlands	JN159518
<i>C. campanulatus</i>	Coprinellus_sp._SHP144	Pakistan	MH753666
	Coprinellus_sp._SH144T	Pakistan	MH753667
<i>C. cinereopallidus</i>	NL-0177	Hungary	HQ847001
	Ulje1163	Netherlands	JN159524
<i>C. congregates</i>	NL-0588	Sweden	FM878013
	NL-2138	Hungary	JN159554
	NL-1221	Hungary	JN159550
	NL-1433	Hungary	JN159552
<i>C. curtus</i>	NL-1490	Hungary	JN159569
	NL-2339	Sweden	FM878016
	NL-1023	Hungary	JN159568
<i>C. deminutus</i>	NL-0761	Hungary	JN159572
<i>C. disseminatisimilis</i>	Coprinellus_sp._SH15	Pakistan	MH753668
	Coprinellus_sp._Cr_3wT	Pakistan	MH753670
	Coprinellus_sp._Cr_3b	Pakistan	MH753669
<i>C. disseminates</i>	NL-2337	Sweden	FM878017
	NL-0786	Hungary	JN159560
	NL-3401	Hungary	JN159561
<i>C. domesticus</i>	Cervenka286	Hungary	HQ847043
	TOK21808	Netherlands	JN159580
<i>C. eurysporus</i>	NL-1761	Hungary	HQ846992
<i>C. flocculosus</i>	NL-0838	Hungary	JN159573
	NL-1567	Hungary	JN159575
	NL-1661	Norway	FN396138
<i>C. flocculosus</i> (as <i>Coprinus</i> "maysoidisporus")	FVDB1743	Hungary	JN159574
<i>C. fuscocystidiatus</i>	NL-2720	Norway	HQ846977
	NL-3622	Sweden	JN159514
<i>C. hiascens</i>	NL-1349	Hungary	JN159525
	NL-2536	Norway	FM878018
	NL-1350	Hungary	GU227720
	NL-2598	Hungary	JN159526
<i>C. impatiens</i>	NL-1164	Hungary	FM163177
	NL-0568	Hungary	JN159511

TABLE 1, continued on p. 324

TABLE 1, continued

SPECIES	VOUCHER	COUNTRY	ITS #
<i>C. micaceus</i>	NL-3888	Hungary	GU227721
	NL-3656	Hungary	JN159567
	NL-1939	Hungary	FN396104
	NL-4253	Hungary	JN159566
	NL-2739	Hungary	JN159564
	NL-2744	Hungary	JN159565
[as <i>C. sp.</i> 10 LGN-2011 in GenBank & <i>C. "xylophilus"</i> in Nagy & al. 2011]	FVBD1726	Hungary	JN159563
*<i>C. ovatus</i>	LAH35939	Pakistan	MK764023
<i>C. pakistanicus</i>	LAH35322	Pakistan	MH366735
	LAH35323	Pakistan	MH366736
	LAH35324	Pakistan	MH366737
<i>C. pallidus</i>	NL-1556	Hungary	JN159521
	NL-0625	Hungary	HQ846989
	NL-4218	Hungary	JN159522
<i>C. pellucidus</i>	NL-1076	Hungary	GU227713
	NL-2928	Slovakia	GU227714
	NL-2344	Hungary	FM878023
<i>C. plagioporus</i>	NL-1365	Hungary	HQ846981
	NL-1086	Hungary	JN159512
<i>C. radians</i>	NL-1373	Sweden	JN159579
	NL-3896	Sweden	HQ847045
<i>C. radicellus</i>	NL-3168	Sweden	GU227719
	NL-0594	Sweden	GU227716
	NL-0957	Norway	GU227718
	NL-2121	Sweden	GU227717
<i>Coprinellus sabulicola</i>	NL-1560	Hungary	JN159557
	NL-2906	Hungary	JN159558
	NL-1027	Hungary	JN159559
	NL-1763	Hungary	HQ847007
<i>C. sassii</i>	NL-1495	Hungary	FN396101
	NL-1237	Hungary	JN159509
<i>C. sclerocystidiosus</i>	NL-0797	Hungary	JN159539
	NL-1022	Hungary	JN159538
	NL-1761	Hungary	HQ846992
	NL-1444	Hungary	JN159537
<i>C. silvaticus</i>	NL-3035	Hungary	HQ846986
<i>C. subimpatiens</i>	ToK 27/8-08	Hungary	HQ846993
	NL-0162	Hungary	JN159542
	Uljé 1191	Netherlands	HQ846995
<i>C. tenuis</i>	Coprinellus _sp._SHP10	Pakistan	MH753663
	Coprinellus _sp._SH10T	Pakistan	MH753664
<i>C. truncorum</i>	NL-1101	Hungary	JN159562
	NL-1294	Sweden	FM878007
<i>C. uljei</i>	NL-2492	Sweden	JN159513
	NL-0157	Sweden	HQ846982
	NL-3985	Slovakia	JN159515
<i>C. verrucispermus</i>	NL-2146	Hungary	JN159577
<i>C. xanthothrix</i>	TOK12808	Netherlands	JN159578
	NL-3417	Hungary	HQ847044
<i>Psathyrella candolleana</i>	NFP-MU1	India	KT443864

* Species information in bold face represents data generated during this study.

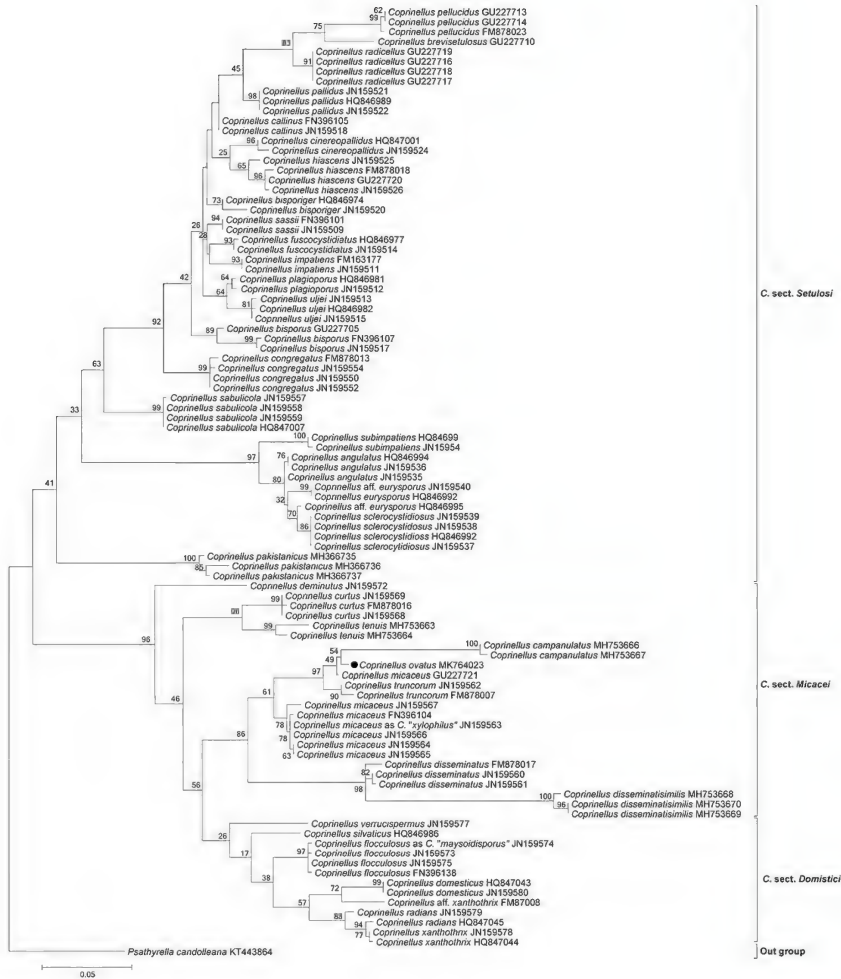


FIGURE 1. Molecular phylogenetic analysis of *Coprinellus* spp. based in ITS sequences. The tree with the highest log likelihood (-5095.2205) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial trees for the heuristic search were obtained by applying the Neighbor-Joining method to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories; +G, parameter = 0.2939). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 96 nucleotide sequences. The sequence generated from LAH35939 is marked with ●.

and July the wettest (https://en.wikipedia.org/wiki/Climate_of_Islamabad; Peel & al. 2007, Belda & al. 2014).

Basidiomata were tagged, photographed, and dried. Morphological features (size, shape, and color) of basidiomata were noted in the field. Color was coded following Munsell (1975). Tissues were mounted in 2% aqueous KOH (w/v) solution for anatomical study and examined using a China XSZ-107-BN light microscope. At least 20 measurements were recorded for each anatomical feature. Basidiospore measurements were taken as: length range $\times$ width range $\times$ breadth range, with outliers shown in parentheses; Q values designate length/width ratios, with Qav = the average Q value. The specimens are deposited at the Herbarium, Department of Botany, University of the Punjab, Lahore, Pakistan (LAH).

DNA was extracted using Extract-N-Amp™ Plant Tissue PCR Kit following manufacturer's instructions. PCR amplification and sequencing were commercially performed by TsingKe, P.R. China.

For phylogenetic analysis, the ITS sequences generated from the Pakistani collections were compared with other sequences in GenBank using Basic Local Alignment Search Tool (BLAST) at NCBI (<https://www.ncbi.nlm.nih.gov/>). Closely matching sequences and those cited in Hussain & al. (2018b) were downloaded from the GenBank for phylogenetic analysis. *Psathyrella candolleana* (Fr.) Maire (HQ847040) was chosen as an outgroup (Hussain & al. 2018b). Sequences were aligned using online MUSCLE tool (<http://www.ebi.ac.uk/>). Best model selection approach was employed on the final data set and Maximum Likelihood (ML) analysis was performed by using Tamura-Nei model (Tamura & Nei 1993) in MEGA 6 (Tamura & al. 2013). The phylogenetic tree was constructed at one thousand rapid bootstrap replicates.

Molecular phylogenetic results

The sequences from specimens used for the molecular phylogenetic analysis are given TABLE 1. The final ITS dataset comprised 96 nucleotide sequences, with 697 positions after trimming from both ends. The resultant phylogenetic tree (FIGURE 1) places the *Coprinellus* sequences in several distinct clades that more or less correspond to previous studies (Nagy & al. 2012, Hussain & al. 2018b). The sequence generated from LAH35939 clustered in *C. sect. Micacei*.

Taxonomy

***Coprinellus ovatus* Kamran & Jabeen, sp. nov.**

FIGURES 2, 3

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Differs from *Coprinellus campanulatus* by its ovate fibrillose pileus, brownish black hymenium, caespitose stipe base, larger mitriform, amygdaliform, and ellipsoid basidiospores, crystal-bearing utriform cheilocystidia, and loosely arranged clavate to mucronate pileipellis hyphae.



FIGURE. 2. *Coprinellus ovatus* (holotype, LAH35939). Basidiomata.
Scale bars: A = 1 cm; B, C = 0.2 cm. Photographs by Muhammad Kamran.

TYPE: Pakistan, Islamabad, on soil under broadleaf trees, 1 May 2018, Muhammad Kamran K4 (LAH35939).

ETYMOLOGY: The specific epithet (L.) refers to oval shape of the pileus.

PILEUS 9–13 × 14–17 mm, ovoid to parabolic, with plane center, orange yellow color (10YR8/8), surface fibrillose, deeply plicate from center to margin. LAMELLAE 1.5–2.5 mm wide, free, entire, crowded, brownish black (10YR2/3). LAMELLULAE absent. STIPE 1.4–2.7 × 2–4 mm, central, smooth radicating, base 3–5 mm wide, yellowish brown (10YR7/8), caespitose, dry, fibrillose. ANNULUS absent. ODOR not observed.

BASIDIOSPORES (8.6–)9.6–11.4(–11.6) × (5.7–)6.0–7.5(–7.8) × (5–)5.6–6. (–7.2) µm, average = 10.5 × 6.7 × 6.0 µm, Q_{av} = 1.5, mitriform or triangular to ellipsoid in face view, amygdaliform to ellipsoid in side view, dark brown to blackish brown in KOH, apiculus prominent, with central germ-pore (2.2–3.0 µm). BASIDIA (17.3–)21.8–36.9(–41.7) × (7–)8.25–10.6(–11) µm, cylindrical, clavate to subclavate, hyaline. CHEILOCYSTIDIA 20–29.3 × 9.2–12.1 µm, utriform, and apex usually bears crystals. PLEUROCYSTIDIA absent. PILEIPELLIS an epithelium of loosely arranged hyphae with clavate to mucronate terminals (51–)55.5–68(–94) × (14–)20–28(–67) µm. UNIVERSAL VEIL ELEMENTS 19.4–44.2 µm wide, globose to subglobose with filament 9.4–26.2 µm. STIPITIPPELLIS (3.2–)11.9–22.9(–29.5) µm, filamentous with frequent septa, with rare clamp connections.

ECOLOGY & DISTRIBUTION—Among broadleaf trees including *Morus* sp.

Discussion

Coprinellus ovatus is phylogenetically most closely related to *C. campanulatus* and *C. truncorum*. *Coprinellus campanulatus* is separated morphologically by a campanulate pileus, pale orange-yellow to dark yellowish-brown lamellae, the presence of lamellulae, smaller basidiospores, larger cheilocystidia, and a pileipellis that is an epithelium of loosely arranged globose to subglobose pileocystidia (Hussain & al. 2018b). *Coprinellus truncorum* differs in the presence of lamellulae and smaller ellipsoid basidiospores that are not distinctly lentiform (Keirle & al. 2004, Uljé 2005).

Coprinellus micaceus differs in its closely crowded adnexed to free lamellae and smaller basidiospores that are lacrimiform to submitriform or mitriform in face view, and conical towards the base (Keirle & al. 2004, Uljé 2005).

Coprinellus ovatus also differs from three recently described species from Pakistan. *Coprinellus disseminatisimilis* is diagnosed by its pruinose parabolic to umbo-campanulate pileus, sinuate to uncinuate lamellae, the presence of lamellulae, ellipsoid to cylindrical/obovoid basidiospores, much larger narrowly clavate to utriform cheilocystidia, and a loosely arranged euhymeniderm pileipellis with more or less utriform pileocystidia (Hussain

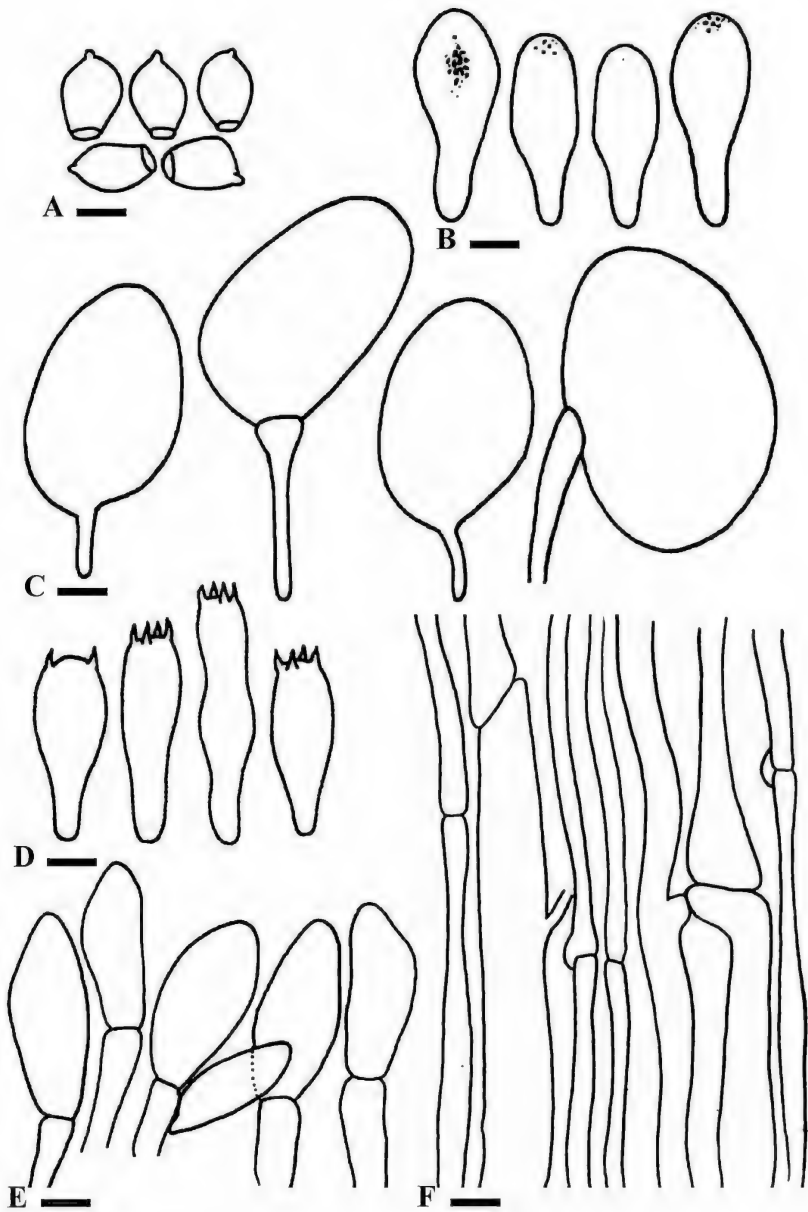


FIGURE. 3. *Coprinellus ovatus* (holotype, LAH35939). A. Basidiospores; B. Cheilocystidia; C. Universal veil elements; D. Basidia; E. Pileipellis hyphae with clavate to mucronate terminals; F. Stipitipellis. Scale bars: A–D = 6 μ m; E, F = 15 μ m. Drawing by Sana Jabeen.

& al. 2018b). *Coprinellus pakistanicus* differs by its convex to plane pileus, the presence of lamellulae, slightly smaller basidiospores, larger cheilocystidia; and the presence of true lageniform/cylindrical pileocystidia (Hussain & al. 2018b). *Coprinellus tenuis*, which produces similar basidiospores, is separated by its convex to plane pileus, sinuate to uncinat lamellae, presence of lamellulae, equal cylindrical stipe, and the presence of lageniform to cylindrical pileocystidia (Hussain & al. 2018b).

TABLE 2. Comparison of *Coprinellus ovatus* and related species.

<i>Coprinellus</i> sp.	PILEUS (mm); Shape; Surface	LAMELLAR ATTACHMENT (lamellulae)	BASIDIOSPORES (μ m) F = face view S = side view	PILEIPELLIS type (terminal cells)	CHEILO- CYSTIDIA (μ m)
<i>ovatus</i>	9–13 $\times$ 14–17; Ovoid to parabolic; Fibrillose	Free, (absent)	9.6–11.4 $\times$ 6–7.5 F: mitriform / ellipsoid; S: amygdaliform / ellipsoid	Loose epithelium (clavate / mucronate)	20–29.3 $\times$ 9.2–12.1
<i>campanulatus</i>	$\leq$ 40 $\times$ 15 Yg: ovoid / parabolic, later campanulate; Pruinose to granulose	Adnexed, (present, 1–4 series)	8–10.5 $\times$ 5.5–6.5 F: mitriform / ellipsoid; S: cylindrical, amygdaliform / ellipsoid	Loose epithelium (globose to subglobose elements)	36–47 $\times$ 35–45
<i>disseminati- similis</i>	$\leq$ 20 $\times$ 20; Parabolic then campanulate; Pruinose to pulverulent	Sinuate to uncinate, (present, 0–2 series)	8–9 $\times$ 5–5.5 F: ellipsoid to cylindrical; S: amygdaliform / ellipsoid	Loose euhymeniderm; (utriform pileocystidia)	70–165 $\times$ 11–15
<i>micaceus</i>	* $\leq$ 24 mm diam; Obtuse cylindrical, then convex / campanulate; white mica- like; granular, detersile	Adnexed or free (absent)	6.5–10 $\times$ 4.5–7 F: lacrimiform to mitriform; conical towards the base	* Epithelium (globose cells)	* 30–40 $\times$ 20–25
<i>pakistanicus</i>	$\leq$ 35 mm; Convex to plane, disc depressed; Smooth, pulverulent, granulose	Free (present, 0–2 series)	8.5–11.5 $\times$ 6.5–8; F: obovoid to phaseoliform; S: ellipsoid to obovoid	Irregular epithelium (lageniform to cylindrical; tapering neck, obtuse apex)	42–75 $\times$ 14–25
<i>tenuis</i>	$\leq$ 20 mm; Pulvinate, convex, plane; Glabrous, furred	Sinuate to uncinate (present, 0–2 series)	10.5–14.5 $\times$ 8–9.5; F: ellipsoid to ovoid S: sl. pyriform to ellipsoid	Loose epithelium (lageniform to obtuse long cylindrical)	22–30 $\times$ 19–28
<i>truncorum</i>	* $\leq$ 14 mm; Oval then convex; finely plicate, granular or with mica-like flecks	* Adnexed or free (present, 1–4 series)	8.5–9 $\times$ 5.5–6; Ellipsoid in all views, not truly lenticiform	* Loose epithelium ([sub]globose to broadly clavate)	* 25–40 $\times$ 25–30

* Reference for *C. micaceus* and *C. truncorum*: Keirle & al. 2004

Full dimensions and comparative characters of the *Coprinellus* species cited above are given in TABLE 2. Although *C. ovatus* is in *C. sect. Micacei*, it is sister to *C. micaceus* and forms a subclade with *C. truncorum* and *C. campanulatus*. *Coprinellus micaceus* sequence (GU227721) from Hungarian collection (NL-3888) also clustered in the same clade with *C. ovatus*, this specimen showed 99.2% sequence similarity and 0.6% divergence from *C. ovatus*. No morphological data is available from this specimen. Since *C. ovatus* showed remarkable morphological differences from *C. micaceus* (Keirle & al. 2004, Uljé 2005), we conclude that LAH35939 represents a new species in *C. sect. Micacei*.

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An update of G.K. Merrill's 1909 "Lichen notes no. 14"

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ABSTRACT—G.K. Merrill proposed three new *Calicium* taxa that have largely been absent from North American lichen literature since their publication in *THE BRYOLOGIST* in 1909. *Calicium obscurum* [= *Chaenotheca obscura*], which colonizes the basidiocarps of *Trichaptum abietinum*, predates the use of *Chaenotheca balsamconensis*. *Calicium minutissimum* was reintroduced as a member of the North American calicioid biota in 1999. *Calicium curtisii* var. *splendidulum* [as "*splendidula*"] is within the range of morphological variation of *Phaeocalicium curtisii* and does not warrant varietal status.

KEY WORDS — *Caliciales*, Maine, pin fungi, stubble lichens

In his Lichen Notes No. 14, G.K. Merrill (1909) described three new *Calicium* taxa: two new species, *C. obscurum* and *C. minutissimum*, and one new variety, *C. curtisii* var. *splendidulum* [as "*splendidula*"]. All three were collected within 30 miles of Penobscot Bay in Knox County, Maine. *Calicium obscurum* was included in Merrill's (1909–13) *Lichenes Exsiccati* as #92, and *C. curtisii* var. *splendidulum* as #24.

Calicium obscurum G. Merr., *Bryologist* 12: 107. 1909

FIG. 1A,B

≡ *Chaenotheca obscura* (G. Merr.) Nád. & Stud. Bot. Cech. 5: 123. 1942

= *Chaenotheca balsamconensis* J.L. Allen & McMullin, *Bryologist* 118: 55. 2015

Calicium obscurum was collected "on dead Polyporei," which we have identified as *Trichaptum abietinum* (Pers. ex J.F. Gmel.) Ryvarden, growing on young pines in Rockland, Maine (FIG. 1A). Two species of algae were reported to be growing with it: *Cystococcus*, better known today as *Trebouxia*,

the photobiont of *C. obscurum*, and “a cylindrical articulated form that I am unable to name” (Merrill 1909). This unknown alga is *Stichococcus*, which commonly grows on the surface of *T. abietinum*. Merrill refers to a second *Calicium*, also growing “on a *Polyporus* on Hemlock Spruce,” that was collected by Willey (1892) “and identified by Tuckerman as *Calicium trichiale*” [≡ *Chaenotheca trichialis* (Ach.) Th. Fr.]. He wondered if the Willey specimen might prove to represent *C. obscurum*, which differs from *C. trichiale* by its lack of a thallus, two forms of algae, and the absence of pruina.

One species that has been erroneously reported from *Trichaptum* in North America is *Chaenotheca brunneola* (Ach.) Müll. Arg. Tibell (1980, 1999) reported finding it occasionally “on old polypores” in Europe, and Fries (1865) noted a *Trichaptum*-dwelling variant which he named as *Ch. brunneola* β *cilians* Th. Fr. This variety, which may be the earliest valid name for *Ch. obscura*, has no priority at species rank; moreover, according to Tibell (1981) and Sujja & al. (2016, and personal communication), the type material of the variety has not been located. Hutchison (1987, p. 789) erroneously cited *Calicium obscurum* as a synonym of *Ch. brunneola*, and Keissler (1938, p. 597) erroneously cited *Calicium obscurum* as a synonym of *Phaeocalicium polyporaeum*. Keissler stated that Muraschinskij had sent him a specimen collected on *Polystictus pergamenus* (Fr.) Cooke [= *Trichaptum biforme* (Fr.) Ryvarden] from Siberia, “which is identical to *Calicium polyporaeum* Nyl.” [≡ *Phaeocalicium polyporaeum* (Nyl.) Tibell] “that is also found in North America under the synonym *Calicium obscurum* Merr.” In North America, *P. polyporaeum* is most commonly found on *T. biforme*, while *Ch. obscura* has, to date, been collected only on *T. abietinum*.

According to Selva (2014), four species of calicioid lichens and fungi have been collected on *T. abietinum* in northeastern North America: *Chaenotheca ferruginea* (Turner) Mig., *Ch. trichialis*, *Chaenothecopsis pusiola* (Ach.) Vain., and *Phaeocalicium polyporaeum*. Allen & McMullin (2015) argued that *Ch. ferruginea* is a corticolous and lignicolous species that does not colonize *Trichaptum abietinum*. They proposed the name *Chaenotheca balsamconensis* for the species that Selva (2014) recorded as *Ch. ferruginea* growing on *T. abietinum*. The two species are remarkably similar, but *Ch. balsamconensis* differs in having smooth rather than ornamented to fissured spores, in often having a KOH+ magenta compound in the stalk, and in having a predominantly endosubstratic thallus. After reviewing an isotype of *C. obscurum* (Merrill exsiccata #92 [CANL]), we found it to be

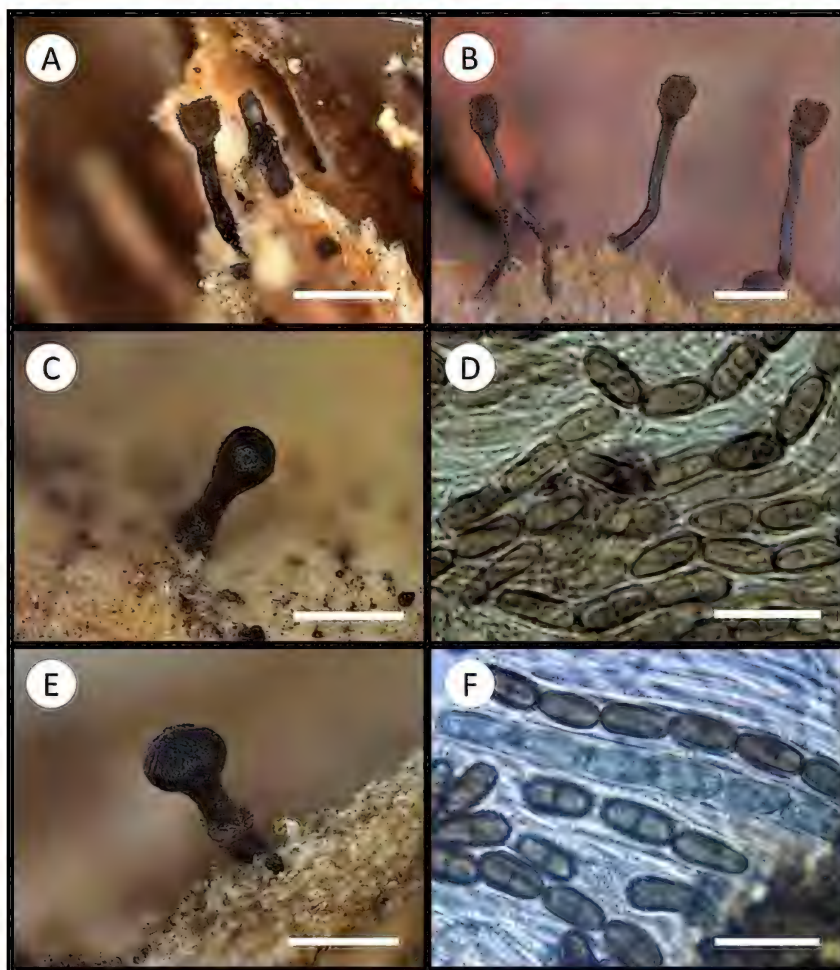


FIG. 1. *Chaenotheca obscura*: A. Apothecia (*Calicium obscurum* isotype, Merrill exsicc. #92, CANL); B. Apothecia (McMullin 16823, CANL). *Phaeocalicium curtisii*. C. Apothecia (*Calicium curtisii* var. *splendidulum* isotype, Merrill exsicc. #24, CANL); D. Ascospores (Merrill exsicc. #24, CANL); E. Apothecia (McMullin 14102, CANL); F. Ascospores (McMullin 20101, CANL). Scale bars: A, B = 0.5 mm; C, E = 0.2 mm; D, F = 20 μ m

conspecific with *Ch. balsamconensis* (FIG. 1A-B), the chemotype lacking the KOH+ magenta stalk. Since *C. obscurum* is a validly published name for this taxon, it should be resurrected. After its publication by Merrill in 1909, the name has never appeared on any of the North American lichen checklists

and seems to have been lost from North American lichen literature. Coincidentally, the same fate befell the two other *Calicium* taxa published in Merrill (1909).

Calicium minutissimum G. Merr., Bryologist 12: 107. 1909

≡ *Phaeocalicium minutissimum* (G. Merr.) Selva, Bryologist 102: 390.

Calicium minutissimum was not recognized as a member of the North American calicioid biota until it was reintroduced by Selva & Tibell (1999). They transferred it to *Phaeocalicium* and, because the type specimen was no longer recognizable, designated a neotype. The original type was first collected by Merrill (1909) on the smooth bark of *Quercus rubra* L. at the summit of Mt. Battie in Camden Hills State Park, Knox County, Maine. The type locality remained the only known location for 90 years until Selva & Tibell (1999) expanded the range to include additional locations in New Brunswick, Maine, New Hampshire, and Vermont. It was later reported from Ontario, Quebec, and Massachusetts by Selva (2010).

Calicium curtisii* var. *splendidulum G. Merr., Bryologist 12: 107. 1909

[as “*splendidula*”]

FIG. 1C–F

= *Calicium curtisii* Tuck., Amer. J. Sci. Arts, Ser. 2, 28: 201. 1859 [var. *curtisii*]

≡ *Phaeocalicium curtisii* (Tuck.) Tibell, Symb. Bot. Upsal. 21(2): 58. 1975

Calicium curtisii var. *splendidulum* was collected on the main stems and larger branches of *Rhus typhina* L. in Rockland, Maine, and on the same substrate in Ottawa, Ontario (Merrill 1909) (FIG. 1C). Tibell (1975) transferred the species to *Phaeocalicium*. The description does not clearly state the characteristics that distinguish *C. curtisii* var. *splendidulum* from the autonomous variety, and the average height of the apothecia and the ascospore measurements fall within those known for the species (FIG. 1C–F). Merrill reported that the ascospores are “simple or indistinctly bilocular;” however, all ascospores observed in an isotype (Merrill exsiccati #24 [CANL]) were clearly 2-celled (FIG. 1D). Merrill also reported that the “capitula are turbinate to subglobose,” a character common in young apothecia (FIG. 1C, E). We propose that *C. curtisii* var. *splendidulum* does not significantly differ from *Phaeocalicium curtisii* and does not warrant varietal status. Fink (1935), who also came to a similar conclusion, did not provide any discussion or reason for synonymizing the variety.

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***Elaphomyces citrinus* and *E. cyanosporus*, new for Turkey**

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ABSTRACT—The first records of two black *Elaphomyces*, *E. citrinus* and *E. cyanosporus*, are reported from Turkey. Short descriptions, photographs, and comments are provided.

KEY WORDS — biodiversity, *Elaphomycetaceae*, hypogeous ascomycetes, sequestrate, truffle-like fungi

Introduction

Elaphomyces T. Nees, “the deer fungus,” is a sequestrate genus in *Elaphomycetaceae*. Its species are characterized by globose to subglobose or irregular hypogeous ascomata that have a fleshy to leathery and smooth to variously warty brown to dark blue or black peridium; a single chambered gleba comprising a powdery slate blue, purple-brown, dark brown, grey-black, or black spore mass; globose to subglobose 1–8-spored asci; and subglobose to globose spiny to verrucose spores (Trappe 1979, Castellano & al. 2012, Castellano & Stephens 2017).

Index Fungorum (2018) accepts 73 *Elaphomyces* taxa, of which four—*E. granulatus* Fr., *E. leucocarpus* Vittad., *E. muricatus* Fr., *E. septatus* Vittad.—have been reported from Turkey (Türkoğlu & al. 2015, Uzun & Kaya, 2019a,b). We report Turkish collections of two black *Elaphomyces* species, *E. citrinus* and *E. cyanosporus*. Current checklists (Sesli & Denchev 2014, Solak & al. 2015) and recent research papers (Işık & Türkeku 2017, Kaşık & al. 2017,

Kaya 2015, Kaya & al. 2016, Kaya & Uzun 2018, Sesli 2018, Şelem & al. 2019; Türkecul 2017, Uzun & Kaya 2019c) have not yet reported *E. citrinus* and *E. cyanocephalus* from Turkey. This study aims to contribute additional knowledge to the mycobiota of Turkey.

Materials & methods

The *Elaphomyces* fruit bodies were collected from Rize and Trabzon provinces during 2015–2018. The ascomata were photographed and the ecological data were recorded in the field; macroscopic and microscopic features were measured in the laboratory. The specimens were examined microscopically using a Nikon Eclipse Ci-S trinocular light microscope and Hitachi SU5000 scanning electron microscope and identified by consulting the literature (Pegler & al. 1993; Montecchi & Sarasini 2000; Arroyo & al. 2005; Binion & al. 2008; Saitta & al. 2009; Castellano & al. 2018; Hobart 2012; Paz & al. 2012, 2017). The specimens are preserved in the fungarium of Department of Biology, Science Faculty, Karamanoğlu Mehmetbey University, Karaman, Turkey (KMU).

Taxonomy

Elaphomyces citrinus Vittad. Monogr. Tuberac.: 65 (1831)

FIG. 1

ASCOMA 10–40 mm in diameter, subglobose, usually covered with adherent lemon-yellow mycelium, not easily separating and binding soil particles to form a crust. CORTEX thin, composed of heavily carbonized dark brown hyphae. PERIDIUM 1–2 mm thick, with a thinner black outer cortex and a dark grey layer below, with a tissue of filamentous hyphae. GLEBA a grey-dark brown powder of thin-walled hyphae. ASCI globose, 8-spored. ASCOSPORES 10.5–12.5 µm in diameter, globose, dark brown when ripe, lightly aculeate-roughish, ornamented with fine anastomosed 0.5–1.5 µm high rods or ridges that form an irregular labyrinthine pattern.

SPECIMENS EXAMINED—TURKEY, TRABZON: Tonya, Hoşarlı village, 40°56'N 39°10'E, 1100 m, mixed forest, in soil under *Castanea sativa* Mill. and *Fagus orientalis* Lipsky, 17.09.2015, Y.Uzun 4537 (KMU); Köprübaşı, Yağmurlu village, 40°49'N 40°07'E, 420 m, mixed forest, under *Corylus avellana* L. and *F. orientalis*, 11.09.2017, Y.Uzun 5821 (KMU).

COMMENTS—In general, the macro- and micromorphological characteristics of our Turkish materials agree with *Elaphomyces citrinus* as described in the literature (Pegler & al. 1993, Saitta & al. 2009, Paz & al. 2012). The bright yellow mycelial crust is reported to be diagnostic of this species (Pegler & al. 1993, Montecchi & Sarasini 2000, Arroyo & al. 2005, Paz & al. 2017). *Elaphomyces cibulae* Castellano & al., also possesses a carbonized outer peridium and similar spore characters, but its white to ivory mycelial crust



FIG 1. *Elaphomyces citrinus* (KMU, Uzun 4537).

a. Ascomata; b. Ascospores; c. SEM image of an ascospore. Scale bar: b = 10 μ m.

and thicker peridial layer distinguish *E. cibulae* from *E. citrinus* (Castellano & al. 2018).

Elaphomyces cyanosporus Tul. & C. Tul, Fungi Hypog.: 113 (1851)

FIG. 2

ASCOMA 15–30 mm in diameter, globose to ovoid, dark brown to black, covered with blackish, thin, irregularly warty cortex. PERIDIUM thick and double layered, the outer layer light brown with whitish and reddish tones, the darker inner layer almost equal in thickness with the outer layer. GLEBA felty and grey when young, firm, turquoise to blackish blue at maturity. ASCI globose 60–80 μ m in diameter with thin hyaline walls. ASCOSPORES 22–26 μ m including ornamentation, globose, turquoise to black, ornamentation almost 2.5 μ m high, forming a fine reticulum with coarse ridges.

SPECIMENS EXAMINED—TURKEY, RIZE: Ardeşen, Kirazlık village, 41°07'N 41°05'E, in soil under *Fagus orientalis* and *Rhododendron ponticum* L., 600 m, 08.08.2016, Y.Uzun 5207 (KMU); TRABZON: Sürmene, Ormanseven village, 40°50'N 40°09'E, in soil under *F. orientalis* and *Carpinus betulus* L., 695 m, 07.07.2018, Y.Uzun 6660 (KMU); Yomra, İkisü village, 40°55'N 39°47'E, in soil under *F. orientalis* and *R. ponticum*, 280 m, 08.07.2018, Y.Uzun 6667 (KMU); Beşikdüzü, Oğuz village, 41°01'N 39°09'E, in soil under *Castanea sativa* and *R. ponticum*, 740 m, 26.08.2018, Y.Uzun 6687 (KMU).

COMMENTS—*Elaphomyces cyanosporus* is a distinctive species with its blue-green tinged inner peridium and spores (Montecchi & Sarasini 2000, Binion & al. 2008, Hobart 2012). It is one of the reticulate-spored members of the genus



FIG 2. *Elaphomyces cyanosporus* (KMU, Uzun 6667).

a. Ascomata; b, c. Asci and ascospores; d. SEM image of an ascospore.

Scale bars: b, c = 20 µm.

(Zhang 1991, Castellano & al. 2016), and the reticulate spore ornamentation of our samples fits well with Castellano & al. (2018). *Elaphomyces persoonii* Vittad., which also has a black warty peridium and similar reticulate spore ornamentation, differs from *E. cyanosporus* by its taller alveoli walls and larger spores (Castellano & al. 2018).

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New records of graphidoid and thelotremoid lichens from India

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ABSTRACT—*Chapsa cinchonarum*, *C. farinosa*, *Diorygma sticticum*, *Fissurina albocinerea*, *Graphis bungartzii*, *G. discarpa*, *G. nigririmis*, *Ocellularia alba*, *Phaeographis pseudostromatica*, *Sarcographa verrucosa*, and *Thelotrema crassisporem* are described and illustrated as new records for India.

KEY WORDS —lichenized fungi, *Graphidaceae*, *Ostropales*, taxonomy

Introduction

Graphidaceae (sensu Rivas Plata & al. 2012) is the largest family of tropical crustose lichens with about 2700 accepted species world-wide (Lücking & al. 2014, 2017a,b); it includes the previously separated, well-known families *Graphidaceae* and *Thelotremataceae*. Kraichak & al. (2018) resurrected *Diploschistaceae* and *Thelotremataceae* which were previously synonymized under *Graphidaceae* and accepted the family *Fissurinaceae* proposed by Hodgkinson (2012).

Here we use *Graphidaceae* sensu Rivas Plata & al. (2012). The family is characterized by: crustose thallus with a trentepohlioid photobiont; lirellate to rounded ascomata; carbonized or non-carbonized proper exciple; interspersed or non-interspersed hymenium; presence or absence of periphysoids; hyaline to brown, transversely septate to muriform ascospores often with amyloid

septa, lens-shaped to rectangular lumina, and the presence or absence of lichen compounds. A total of 570 graphidoid and 131 thelotremoid species were known from India (Singh & Sinha 2010, Sinha & al. 2018). During the study of *Graphidaceae* specimens available in the herbarium of the National Botanical Research Institute, Lucknow, India (LWG), eleven more species were identified as new to India. They are described below.

Material & methods

Morphological observations were made using the Leica S8APO stereomicroscope with image analyzer software. Thin, hand-cut sections of the thalli and ascomata were mounted in water, lactophenol cotton blue, 10% KOH, or Lugol's iodine solution and observed under the Leica DM2500 compound microscope. All anatomical measurements were taken in water mounts. Secondary metabolites were identified by thin layer chromatography (TLC) following Orange & al. (2010). The examined specimens are preserved in the herbarium LWG.

New records

Chapsa cinchonarum (Fée) Frisch, Biblioth. Lichenol. 92: 95 (2006) FIG. 1A

Thallus crustose, corticolous, white to pale greenish-grey, continuous, matte to mealy or faulty, ecorticate; apothecia angular to elongated and often slightly branched, 0.5–0.8 mm long; margin jagged to lobed, slightly incurved to recurved, with a white to pale fawn, compact to felty inner surface; disc pale brown, covered by thick white felty to crystalline pruina; exciple fused, uncarbonized; hymenium hyaline, clear, 70–110 µm high, I–; ascospores 8/ascus, hyaline, fusiform, 8–14-locular, 18–35 × 4–6 µm, I–; lichen substances absent.

SPECIMEN EXAMINED: INDIA. GOA, Cotigao Wildlife Sanctuary, 14°57'11"N 74°09'21"E, on bark, 12 September 2017, Pallavi P. Randive GU L575 (LWG-35879).

COMMENTS—Morphologically *Chapsa cinchonarum* closely resembles *C. alborosella* (Nyl.) Frisch, which differs in having more rounded apothecia with a rim-like margin and 5–9-locular, smaller (17–22 × 4.5–5 µm) ascospores. It somewhat resembles *Astrochapsa platycarpella* (Vain.) Parnmen & al., which possesses 4–7-locular, smaller (12–16 × 3–5 µm) ascospores.

Previously known from tropical Africa and the Neotropics (Frisch & al. 2006, Rivas Plata & al. 2010).

Chapsa farinosa Lücking & Sipman, Phytotaxa 55: 37 (2012) FIG. 1B

Thallus crustose, corticolous, white-grey, distinctly farinose, ecorticate; apothecia erumpent, angular-rounded, 0.2–0.5 mm diam.; disc exposed,

flesh-coloured to pale brown, white-pruinose; margin lobulate to recurved, pale brown, felty white-pruinose; exciple fused, uncarbonized; hymenium hyaline, clear, I–; ascospores 8/ascus, hyaline, fusiform-oblong, with slightly thickened septa and rectangular lumina, 8–10-locular, $20\text{--}32 \times 4\text{--}6 \mu\text{m}$, I–; lichen substances absent.

SPECIMENS EXAMINED: INDIA. GOA, Ta Rivana, Quinamol, $15^{\circ}09'20''\text{N}$ $74^{\circ}06'21''\text{E}$, 2 December 2016, Pallavi P. Randive GU 400, 404 (LWG-35882, 35883).

COMMENTS—*Chapsa farinosa* is characterized by its whitish, farinose thallus lacking any traces of a cortex. *Chapsa cinchonarum* can be easily confused with *C. farinosa* but has a compact thallus with loose cortex and often elongate lirellae. Anatomically, it resembles *C. albida* (Nyl.) Lücking & Sipman but differs in the distinctly verruculose thallus with irregular cortex (Rivas Plata & al. 2010).

Previously known from Costa Rica (Sipman & al. 2012).

Diorygma sticticum Sutjar., Kalb & Lücking, Phytotaxa 18: 49 (2011) FIG. 1C

Thallus crustose, corticolous, light green, smooth to uneven, continuous, ecorticate; apothecia lirellate in dense clusters, stellately branched, erumpent, with thick, complete, white thalline margin, $1\text{--}2.5 \times 0.15\text{--}0.3 \text{ mm}$; disc concealed to partly exposed, pale brown but thickly white-pruinose; exciple conspicuous, uncarbonised, entire, basally orange-brown, upper part hyaline; epihymenium granulose, yellow-brown; hymenium hyaline, clear, I–; ascospores 8/ascus, hyaline, fusiform, submuriform, $10\text{--}15 \times 6\text{--}8 \mu\text{m}$, I+ blue, rarely found; stictic acid present.

SPECIMEN EXAMINED: INDIA. GOA, Cotigao Wildlife Sanctuary, $15^{\circ}01'07''\text{N}$ $74^{\circ}12'33''\text{E}$, on bark, 15 December 2017, Pallavi P. Randive GU 193 (LWG-35880).

COMMENTS—*Diorygma sticticum* is characterized by its small submuriform ascospores and the presence of stictic acid. *Diorygma nothofagi* (A.W. Archer) A.W. Archer and *D. poitaei* (Fée) Kalb & al. are morphologically similar but *D. nothofagi* differs by larger ($18\text{--}23 \mu\text{m}$ long) ascospores and the presence of norstictic acid while *D. poitaei* is distinguished by the larger ($40\text{--}65 \mu\text{m}$ long) ascospores and presence of hypostictic and hypoconstictic acids.

Previously known from Thailand (Kalb & al. 2004, Feuerstein & al. 2014).

Fissurina albocinerea (Vain.) Staiger, Biblioth. Lichenol. 85: 126 (2002) FIG. 1D

Thallus crustose, corticolous, greyish-green, smooth, glossy, corticate; apothecia lirellate, immersed to slightly raised, simple to very rarely branched, $0.4\text{--}2 \text{ mm}$ long, straight to curved, terminally acute; disc sunken, slit-like,

epruinose; exciple entire, uncarbonized, orange-brown; hymenium hyaline, clear, I–; ascospores 8/ascus, hyaline, 4-locular, $16\text{--}18 \times 6\text{--}9\text{ }\mu\text{m}$, I–; psoromic acid present.

SPECIMEN EXAMINED: INDIA. GOA, Cotigao Wildlife Sanctuary, $14^{\circ}58'23''\text{N}$ $74^{\circ}09'36''\text{E}$, on bark, Pallavi P. Randive, GU 99, 108 (LWG-35884).

COMMENTS—*Fissurina albocinerea* belongs to the group of species having *Dumastii*-type ascomata and is clearly distinguished from the other species of this group in having small ascospores and psoromic acid in the thallus.

Previously known from the Philippines (Staiger 2002).

Graphis bungartzii A.B. Peña, Lücking, Herrera-Camp. & R. Miranda, Lichenologist 46: 71 (2014) FIG. 1E

Thallus crustose, corticolous, pale greenish-brown, smooth, continuously corticate; apothecia lirellate, flexuous, branched, erumpent with lateral thalline margin, 1–2.5 mm long, 0.1–0.3 mm wide; labia concealed, striate, black; exciple thick, laterally carbonized, 15–45 μm wide; epithecium brown, granulose; hymenium hyaline, clear, I–; ascospores 8/ascus, hyaline, ellipsoid to fusiform, 4–10-locular, $25\text{--}32 \times 5\text{--}8\text{ }\mu\text{m}$, I+ blue; norstictic and connorstictic acids present.

SPECIMENS EXAMINED: INDIA. ASSAM, Sonitpur district, Panigaon, Miranda, 75 m, 25 February 2013, on *Syzygium cumini* bark, R. Daimari 14-020543, 14-022465, 14-022467 (LWG); Pithakowa, 70 m, 18 March 2012, on *Bombax* sp., R. Daimari 14-022460 (LWG); New Siliguri, 118 m, 21 March 2013, R. Daimari 14-022463 (LWG); Borbhogia, 64 m, on *Lannea grandis* bark, 26 March 2013, R. Daimari 14-022464 (LWG); Ratanjuli, on *Artocarpus heterophyllus* bark, 21 March 2013, R. Daimari 14-020556 (LWG).

COMMENTS—*Graphis bungartzii* differs from *G. elegans* (Sm.) Ach. by the presence of erumpent lirellae with lateral thalline margin and the smaller ascospores. *Graphis filiformis* Adaw. & Makhija is also similar to *G. bungartzii* but differs in having longer, irregularly to radiately branched lirellae with entire labia and in lacking connorstictic acid.

Previously known from Mexico (Barcenas-Peña & al. 2014).

Graphis discarpa A.W. Archer, Mycotaxon 89: 325 (2004) FIG. 1F

Thallus crustose, corticolous, pale olive-green, dull, corticate; apothecia lirellate, numerous, scattered, immersed, simple, straight, curved or sinuous, rarely branched, concealed, $1\text{--}3 \times 0.15\text{--}0.3\text{ mm}$, visible as a thin black line with white margins, separated from the thallus; exciple entire, completely carbonized; hymenium hyaline, clear, I–; ascospores 8/ascus, hyaline, narrowly ellipsoid to fusiform, 8–11-locular, $32\text{--}40 \times 8\text{--}10\text{ }\mu\text{m}$, I+ blue; stictic acid present.

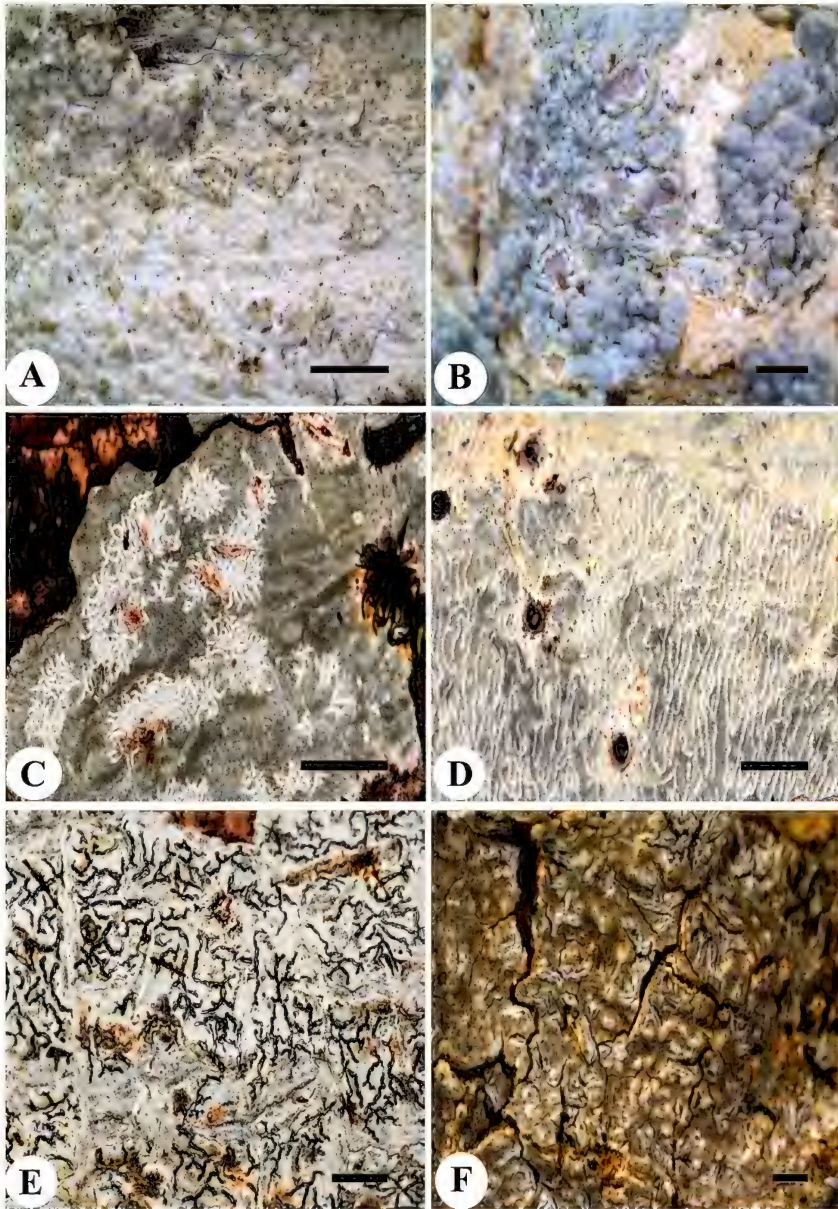


FIG. 1. A. *Chapsa cinchonarum* (LWG-35879); B. *Chapsa farinosa* (LWG-35882); C. *Diorygma sticticum* (LWG-35880); D. *Fissurina albocinerea* (LWG-35884); E. *Graphis bungartzii* (LWG-14-020543); F. *Graphis discarpa* (LWG-14-024670). Scale bars = 1 mm.

SPECIMEN EXAMINED: INDIA. WEST BENGAL, West Medinipur district, Mohunpur, IISER-Kolkata campus, January 2014, T. Hembram, S. Nayaka & S. Asthana 14-024670 (LWG).

COMMENTS—*Graphis discarpa* is closely related to *G. glaucescens* Fée with respect to external morphology but distinguished by its entire to striate exciple, ecorticate, glaucous grey thallus without lichen substances. *Graphis immersella* Müll. Arg., which is also morphologically similar, can be distinguished from *G. discarpa* in having stictic acid and a laterally carbonized exciple.

Previously known from Papua New Guinea (Archer 2004).

***Graphis nigririmis* (Nyl.) Müll. Arg., Bull. Herb. Boissier 3: 320 (1895) FIG. 2A**

Thallus crustose, corticolous, pale olive green, thin, smooth and shiny; apothecia lirellate, inconspicuous, immersed, visible only as a thin black or dark brown line, sometimes becoming conspicuous as black immersed lirellae, simple to branched, 1–3 mm long, 0.05–0.1 mm wide; disc concealed or slightly open; exciple entire, pale orange-brown, weakly apically carbonised; hymenium, hyaline, clear, I–; ascospores 8/ascus, ellipsoid to fusiform, 4–7-locular, 18–25 × 8–16 µm, I+ blue; lichen substances absent.

SPECIMEN EXAMINED: INDIA. TAMIL NADU, Namakkal district, Kolli Hills, 800 m, on bark, 20 March 2016, S. Nayaka & party 16-029294 (LWG).

COMMENTS—*Graphis nigririmis* resembles *G. glaucescens*, which is distinguished by the larger ascospores and the corticated, farinose thallus.

Previously known from Australia (Archer 2009).

***Ocellularia alba* (Fée) Müll. Arg., Mém. Soc. Phys. Genève 29(8): 6 (1887) FIG. 2B**

Thallus crustose, corticolous, white-grey to pale olive, smooth to uneven, with prosoplectenchymatous cortex; apothecia erumpent, rounded, 0.2–0.3 mm diam., eolumellate; disc exposed, pale brown, white-pruinose; margin white pruinose; pores usually small, occasionally broad, to c. 0.2 mm wide, mostly ±rounded to somewhat irregular; exciple usually thin, hyaline internally, pale yellowish to yellowish brown marginally, fused; hymenium hyaline, clear; ascospores 8/ascus, hyaline, fusiform, with slightly thickened septa and rectangular lumina, 4–6-locular, 18–24 × 4–8 µm, I–; lichen substances absent.

SPECIMEN EXAMINED: INDIA. Goa, Cotigao Wildlife Sanctuary, 14°57'11"N 74°09'21"E, on bark, 15 January 2018, Pallavi P. Randive GU 676 (LWG-35881).

COMMENTS—*Ocellularia alba* is morphologically resembles *O. papillata* (Leight.) Zahlbr. and differs in the dark brown exciple and columella.

Previously known from Australia, Brazil, the Philippines (Hale 1978).

Phaeographis pseudostromatica Seavey & J. Seavey, Bull. Florida Mus. Nat. Hist.

53: 228 (2017)

FIG. 2C

Thallus crustose, corticolous, brownish-grey, shiny, continuous; apothecia lirellate, thin, brownish-black, immersed to erumpent, partly branched, 0.2–1 mm long, arranged in broad confluent pseudostromatic areas; disc partly open, brownish-black, epruinose; exciple brown, apically slightly thickened, 20–25 μm wide; epihymenium brown; hymenium hyaline, inspersed; ascospores 8/ascus, brown, fusiform, submuriform, $4\text{--}6 \times 1\text{--}2$ -locular, 22–30 $\times$ 7–10 μm ; norstictic acid present.

SPECIMEN EXAMINED: INDIA. ASSAM, Sonitpur district, Arimora, on Korsun bark, 54 m, 13 March 2012, R. Daimari 14-022470 (LWG).

COMMENTS—*Phaeographis pseudostromatica* is morphologically similar to *P. quadrifera* (Nyl.) Staiger but differs by its lirellae arrangement in pseudostromal tissue. It is also similar to *P. nylanderi* (Vain.) Zahlbr. which shares the inspersed hymenia and the presence of norstictic acid but differs in the transversely septate ascospores and the absence of pseudostromata.

Previously known from Florida (Seavey & al. 2017).

Sarcographa verrucosa (Vain.) Zahlbr., Cat. Lich. Univ. 2: 467 (1924)

FIG. 2D

Thallus crustose, corticolous, olive-brown to yellow-brown, verruculose, corticated; apothecia lirellate, grouped together in white stromata at the thallus level or sunken; thalline margin at edge of the stroma or with extended lirellae; stromata irregularly ovoid, flattened; black, with crowded, open, not confluent or branched, sub-circular, 0.2–0.4 mm long lirellae; disc black, white-pruinose; exciple thin, carbonized or dark brown, 10–15 μm ; epihymenium grey to brownish, granular; hymenium hyaline, inspersed; ascospores 8/ascus, brown, 4–6-locular, $19\text{--}26 \times 6\text{--}8 \mu\text{m}$; stictic acid present.

SPECIMEN EXAMINED: INDIA. ASSAM, Sonitpur district, Choibari, on *Chukrasia tabularis* bark, 81 m, 25 February 2013, R. Daimari 14-022477 (LWG).

COMMENTS—*Sarcographa verrucosa* differs from all other *Sarcographa* species by its olive brown, verruculose thallus, highly inspersed hymenium, submuriform ascospores, and stictic acid chemistry. In having white stroma, white pruinose disc and muriform, brown ascospores, *Sarcographa subtorquescens* (Nyl.) Zahlbr. resembles *S. verrucosa* but differs in having a clear hymenium and larger ($2\text{--}27 \times 9\text{--}11 \mu\text{m}$) ascospores. *Sarcographa labyrinthica* (Ach.) Müll. Arg. and *S. glyphiza* (Nyl.) Kr.P. Singh & G.P. Sinha are also morphologically very similar, but *S. labyrinthica* differs in having transversely septate, 4–6-locular ascospores and a K+ reddish thallus, while

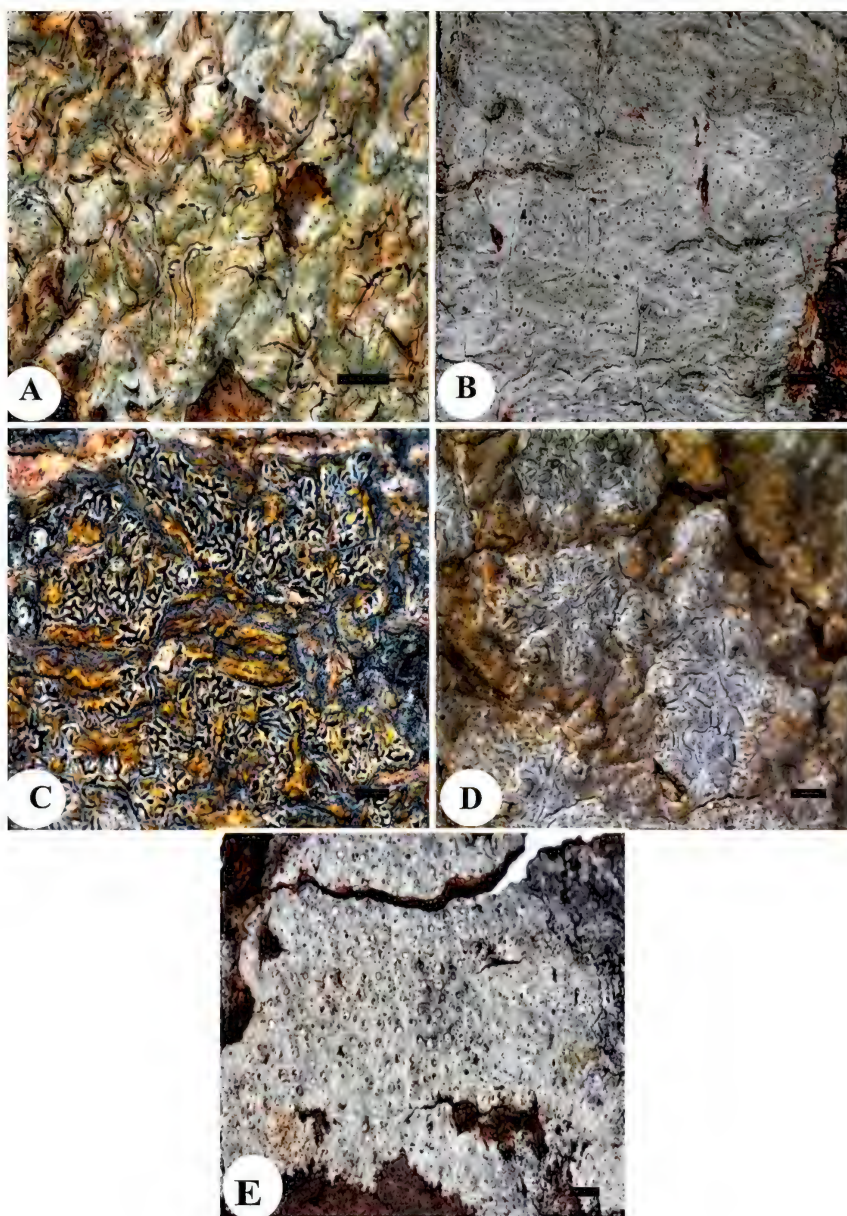


FIG. 2. A. *Graphis nigririmis* (LWG-16-029294); B. *Ocellularia alba* (LWG-35881); C. *Phaeographis pseudostomatica* (LWG-14-022470); D. *Sarcographa verrucosa* (LWG-14-022477); E. *Thelotrema crassisporum* (LWG-35878). Scale bars = 1 mm.

S. glyphiza has larger ($25\text{--}31 \times 9\text{--}13 \mu\text{m}$) ascospores and a K⁺ red thallus with stictic and constictic acid.

Previously known from Australia, Indonesia, and the Philippines (Archer 2009).

Thelotrema crassisporem Mangold, Flora of Australia 57: 657 (2009) FIG. 2E

Thallus crustose, corticolous, pale yellowish grey to pale greenish grey, smooth, continuous, ecorticate; apothecia c. 0.5–0.6 mm diam., ±rounded, solitary to slightly marginally fused, emergent, mostly hemispherical; disc pale greyish, slightly pruinose, invisible from above; pores c. 0.1 mm diam., irregular; exciple completely free, thin, hyaline internally, yellowish brown marginally, apically dark brown; hymenium hyaline, clear; ascospores 8/ascus, hyaline, submuriform, subglobose to ellipsoidal, with ±rounded ends, $4\text{--}7 \times 1\text{--}2$ -locular, $14\text{--}20 \times 8\text{--}10 \mu\text{m}$, I–; constictic and stictic acids present.

SPECIMEN EXAMINED: INDIA. GOA, Cotigao Wildlife Sanctuary, $14^{\circ}57'11''\text{N}$ $74^{\circ}09'21''\text{E}$, on bark, 06 February 2016, Pallavi P. Randive, GU 581 (LWG-35878).

COMMENTS—*Thelotrema crassisporem* is similar to *T. myriocarpum* Fée, which is distinguished by a shiny, smooth, corticated, non-fissured thallus and larger ($\leq 40 \mu\text{m}$ long) ascospores.

Previously known from Australia (Mangold 2009).

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***Carbonea assimilis* and *Rinodina aspersa*, new to Poland**

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ABSTRACT—Two saxicolous species of crustose lichens new to Poland, *Carbonea assimilis* and *Rinodina aspersa*, were recorded from the SW part of the country where there is an abundance of different rock formations, including natural outcrops of volcanic rocks. The characteristics of these species, as well as their ecology and geographical distribution, are provided and briefly discussed.

KEY WORDS—*Ascomycota*, *Lecanoraceae*, *Physciaceae*, taxonomy

Introduction

The lichen biota of Poland (now estimated at c. 1600 species; Fałtynowicz 2003) continues to be enlarged by newly reported taxa, most of which are corticolous, crustose, and especially sorediate lichens, the determination of which has been made possible through the use of thin layer chromatography or phylogenetic analysis (Kukwa & Kubiak 2007; Czarnota & al. 2009; Kukwa & Jabłońska 2009; Kukwa & al. 2012; Guzow-Krzemińska & al. 2016, 2018). Less frequently new records are foliose (Ossowska & al. 2014, Ossowska & Kukwa 2016) or saxicolous species (Wilk & Flakus 2006; Flakus 2007, 2014; Śliwa & Flakus 2011; Wilk 2011).

In this paper, new records of saxicolous species collected from natural outcrops of volcanic rock formations in SW Poland are presented. Volcanic rocks, including basalt rocks, are often habitats for rare lichens and consequently rare lichenicolous fungi (Kossowska 2000; Szczepańska 2012a, 2012b, 2015; Szczepańska & al. 2013) due to specific conditions, usually warm

and dry, as well as a substrate rich in minerals, such as calcium and magnesium compounds.

As the two presented species possess inconspicuous, crustose thalli that could be confused with similar taxa, their diagnostic features are provided as well as habitat requirements and distribution in Central Europe.

Materials & methods

Specimens were collected by the author in 2012 and 2013 during lichenological investigations of natural outcrops of volcanic rocks in the Polish Sudety Mountains. Descriptions of the species are based on the personal observations, measurements, and TLC analyses. The morphology of the species was studied with dissecting and light microscopes following routine techniques; for light microscopy, free-hand sections were made with a razor blade and mounted in water. Tissue measurements were made in water, and ascospore measurements in 10% KOH (K). The TLC analyses were performed in solvent systems A, B, and C, using the standardized method of Culberson (1972) and following Orange & al. (2001). Localities of the species are mapped according to the ATPOL grid square system (Zajac 1978) modified by Cieśliński & Fałtynowicz (1993). Herbarium material is housed in the private herbaria of the author (Hb. Szczepańska), with duplicates donated to the Herbarium, Wrocław University, Wrocław, Poland (WRSL) and to the Herbarium, Gdansk University, Gdansk, Poland (UGDA).

The species

Carbonea assimilis (Hampe ex Körb.) Hafellner & Hertel,

Flecht. Baden-Württembergs, Verbreitungsatlas: 511, 1987.

FIG. 1

THALLUS lichenized, crustose, small and thin, areolate, forming irregular patches between other lichens thalli. PROTHALLUS invisible. AREOLES flat to slightly convex, 0.2–1.0 mm diam., angular, matte to glossy, olive-brown. APOTHECIA sessile, small, 0.1–0.3 mm diam., dispersed, rounded, proper margin persistent, glossy and rather thick, disc black, flat and glossy. HYMENIUM colourless, 40–50 µm tall, epithecium greenish-blue, HYPOTHECIUM colourless, exciple thick, dark, brownish-black, paraphyses simple to slightly branched. ASCI 8-spored, *Lecanora*-type with non-amyloid apical cushion, ocular chamber visible. ASCOSPORES: hyaline, simple, ellipsoid, 8–10 × 5–6 µm.

CHEMISTRY—No chemical substances were detected in the analyzed material.

SPECIMEN EXAMINED—POLAND, SUDETY MOUNTAINS, Pogórze Zachodniosudeckie Foothills, Ostrzyca Proboszczowicka hill, alt. 450 m, ATPOL grid square Eb-40, on basanite rocks, 26 Sept. 2012, K. Szczepańska 939 (Hb. Szczepańska; duplicate in WRSL).

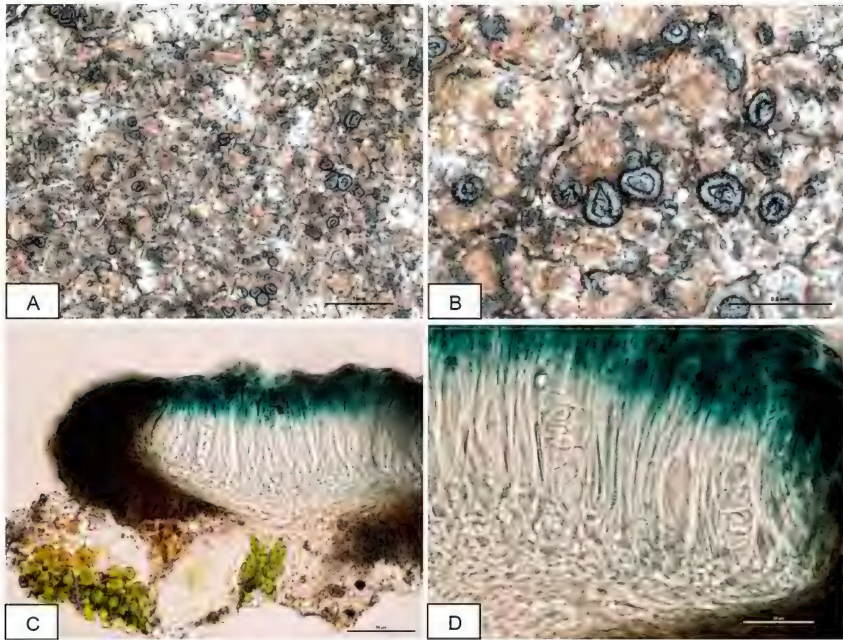


FIG. 1. *Carbonea assimilis* (WRS� – Szczepańska 939): A. thallus; B. apothecia; C. cross section through apothecium; D. ascospores in the ascus. Scale bars: A = 1 mm, B = 0.5 mm, C = 50 µm, D = 20 µm.

ECOLOGY—The species is known as an obligate parasite of crustose lichens. It initially parasitizes various lichen taxa growing on siliceous rocks, such as *Aspicilia* spp., *Lecanora frustulosa*, *Lecidea lapicida*, *Pertusaria pseudocorallina*, *Rhizocarpon* spp., and *Tephromela atra*, before developing independent thalli (Andreev 2003, Hafellner 2006, Pirogov & al. 2014). Typical habitats for *Carbonea assimilis* are neutral to weakly basic, mineral-rich rocks (e.g. basalt, gneiss, and slate), in sunny and warm places, in mountain regions (Wirth 1995, Chambers & al. 2009).

The Polish locality of *Carbonea assimilis* was on a volcanic hill in SW Poland. The hill is one of the relics of ancient volcanic activity in this region, and during the last glaciation it was nunatak (free of ice) (Staffa 2002). In this locality *C. assimilis* was found in a non-parasitic state, growing directly on the rock in an exposed and insolated place. Associated lichen species included *Candelariella vitellina*, *Lecanora soralifera*, *Lecidea fuscoatra*, and *Xanthoparmelia loxodes*.

DISTRIBUTION—*Carbonea assimilis* is considered a widely distributed but rare species, occurring in Europe, Asia, and North America (Andreev 2003). In Europe it has been found in Austria (Hafellner 1997), Czech Republic (Vězda & Liška 1999), Denmark (Søchting & Alstrup 2002), Germany (Wirth 1995), Britain (Smith & al. 2009), France (Roux 2012), Norway (Santesson & al. 2004), Portugal (Boom 1999), Romania (Costache & al. 2007), Spain (Llimona & Hladun 2001), Sweden (Santesson & al. 2004), and Ukraine (Pirogov & al. 2014).

COMMENTS—The genus *Carbonea* (Hertel) Hertel, which was separated from *Lecidea* s. lat. by Hertel (1983), is represented by about 20 species of lichenized and lichenicolous fungi worldwide (Pirogov & al. 2014), of which five were previously known from Poland (Fałtynowicz 2003). Most of these species are exceedingly rare in the country, having scattered localities almost exclusively in the mountainous areas.

The Polish specimen of *Carbonea assimilis* presents this species' typical brown areolate thallus and very small black apothecia (FIG. 1A, B) with characteristic greenish-blue epithecium, dark exciple and colourless hypothecium (FIG. 1C). However, some small differences may be observed in the size of spores (FIG. 1D), which are shorter than cited in the literature data (see Chambers & al. 2009, Pirogov & al. 2014).

Carbonea assimilis can be confused with members of *Lecidella* Körb. Both *Carbonea* and *Lecidella* species usually have black apothecia with a lecideine margin, a blue-green epithecium and *Lecanora*-type asci. *Carbonea* differs mainly in its narrower spores and black true exciple, which in *Lecidella* species is usually pale within. Among *Carbonea* species developing independent, distinct thalli, *C. assimilis* may be confused primarily with *C. vorticosa* (Flörke) Hertel. However, *C. vorticosa* has a grey to whitish thallus, dark brown-black hypothecium, and narrower (4–5 µm diam.) ascospores and mainly grows in high montane regions (Pirogov & al. 2014).

Rinodina aspersa (Borrer) J.R. Laundon, Lichenologist 18: 175. 1986.

FIG. 2

THALLUS small, more or less circular, ≤13 mm diam., composed of aggregated or (more rarely) dispersed, areoles, delimited by a clearly visible, wide black prothallus, ≤0.2 mm. **AREOLES** discrete, rounded to angular, slightly convex, pale to dark grey, matte. **SORALIA** discrete, punctiform to circular, ≤0.3 mm diam., elevated, arising on the surface of the areoles, mainly in the centre of the thallus, concolorous with areoles or slightly grey-green

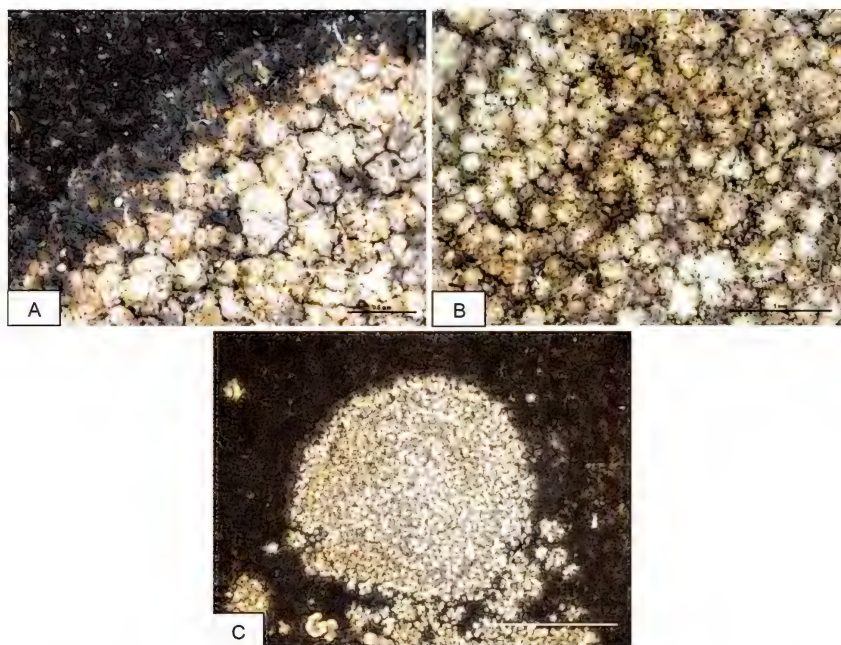


FIG. 2. *Rinodina aspersa* (WRSL – Szczepańska 941): A. prothallus. B. soralia; C. thallus.
Scale bars: A = 0.5 mm, B = 1 mm, C = 5.0 mm.

in shaded places and dark-grey in more exposed habitats. SOREDIA farinose. APOTHECIA not observed in the studied material.

[Additional data from Mayrhofer & Moberg 2002: Apothecia very rare, ≤ 1 mm diam., lecanorine, disc brown to black, plane. Hymenium < 100 μ m tall, epihymenium brown, with fine granules. Hypothecium colourless. Ascospores $15\text{--}20 \times 13\text{--}20$ μ m, *Pachysporaria*-type.]

CHEMISTRY—*Rinodina aspersa* contains atranorin in the cortex (K+ yellow) and additional substances in the medulla, such as gyrophoric (C+ red; usually accompanied by lecanoric and orsellinic acids), umbilicatic, ovoic, and 5-O-methylhiassic acids (Mayrhofer & Moberg 2002). Substances detected in the Polish specimens are consistent with the literature data.

SPECIMEN EXAMINED—POLAND, SUDETY MOUNTAINS, Góry Kamienne Mts, Krucza Skala Mt., alt c. 680 m, ATPOL grid square Eb-91, on volcanic rocks - porphyries, 17 Sept. 2012, K. Szczepańska 941 (Hb. K. Szczepańska; duplicates in UGDA-L and WRSL).

ECOLOGY—Typical habitats of *R. aspersa* in lichenological literature mention humid, foggy, and shaded places (Mayrhofer & Moberg 2002, Motiejūnaitė

& Grochowski 2014), including coastal sites (Giralt & Barbero 1995, Wirth 1995, Giavarini & al. 2009, Sheard 2010). Lime-free, hard silicate rocks (such as basalt, flint, gneiss, granite, shale, and rhyolite) are mentioned as substrata for this species. Very rarely *R. aspersa* has been noted in well-lit or sunny habitats (Vondrák & al. 2006) or on anthropogenic substrata, such as granitic megalithic monuments (Giralt & al. 1997).

The Polish locality of *Rinodina aspersa* lies in SW Poland on the rocky outcrops of a small mountain. Numerous *R. aspersa* thalli were observed on rocks and on stones forming a scree. Associated lichens were *Acarospora fuscata*, *Amandinea punctata*, *Aspicilia cinerea*, and *Lecanora polytrypa*. Habitat conditions here are rather specific, with high insolation and low moisture of the substrates. This newly reported record of *Rinodina aspersa* may indicate a wider ecological spectrum, including not only shaded and humid habitats, but also warm, sunny and dry ones.

DISTRIBUTION—*Rinodina aspersa* is considered a rare species, distributed from temperate Europe to south Portugal and the Mediterranean islands. It is found in the Czech Republic (Vězda & Liška 1999) Denmark (Søchting & Alstrup 2002), Finland (Vitikainen 1997), France (Mayrhofer & Moberg 2002, Roux 2012), Germany (Wirth 1995), Italy (Mayrhofer & Moberg 2002), Lithuania (Motiejūnaitė & Grochowski 2014), Montenegro (Knezevic & Mayrhofer 2009), Netherlands (Aptroot & al. 1999), Portugal (Giralt & Barbero 1995), Spain (Llimona & Hladun 2001), Sweden (Santesson & al. 2004), and U.K. (Smith & al. 2009). It has also been reported from North America (Glew 1999) and Taiwan (Aptroot & Sparrius 2003).

COMMENTS—*Rinodina* (Ach.) Gray is represented by c. 200 species (Giavarini & al. 2009), of which c. 30 are known in Poland (Fałtynowicz 2003). *Rinodina aspersa* adds a fifth sorediate *Rinodina* species to the four previously recorded from Poland (Czarnota & Kukwa 2007, Kukwa & Kubiak 2007). However, unlike the other four species, which are epiphytic, *R. aspersa* occurs only on rocky substrates. In comparison with the other *Rinodina* species noted in Poland, it can be distinguished by its thallus chemistry, especially by the presence of gyrophoric acid, which is absent in other sorediate *Rinodina* species. The chemistry of the thallus and the occurrence of soralia are the most significant characters allowing one to differentiate *R. aspersa* from other species of *Rinodina*. All of the morphological features, as well as the chemistry of the Polish specimen are typical for this taxon and consistent with the descriptions given in the literature (Giralt & al. 1997, Giavarini & al. 2009, Sheard 2010).

Due to the presence of gyrophoric acid in the thallus and soralia (C+ red), *R. aspersa* may be confused with the saxicolous species of *Trapelia* M. Choisy, especially *T. obtegens* that additionally possess a similar thallus composed of scattered, convex areoles. The features that allow one to distinguish the two taxa are the clearly visible, black prothallus (FIG. 2A), discrete soralia (FIG. 2B), and more or less circular thallus of *Rinodina aspersa* (FIG. 2C).

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***Badhamia versicolor* and *Trichia subfusca*, new records for Belarus**

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ABSTRACT—Two myxomycetes, *Badhamia versicolor* and *Trichia subfusca*, are reported for the first time for Belarus. Descriptions and illustrations of both species are provided.

KEY WORDS—biodiversity, Mycetozoa, myxobiota, Protozoa, slime moulds

Introduction

Published accounts of the myxomycetes of Belarus date from the end of the 19th century (Błoński 1888, 1889, 1890; Twardowska 1885). During the ensuing years, the studies of slime moulds were accidental. Important research during the 20th century by Moroz & Novozhilov (1988, 1994) and Moroz (1996) reported 139 species including literature citations and new records. Since then and until very recently (Moroz & Novozhilov 2018; Tsurykau 2017), myxomycetes have been neglected in Belarus.

Recent revision of herbarium material revealed two globally rare myxomycete species new to Belarus, *Badhamia versicolor* and *Trichia subfusca*. The present contribution details their phenotypic characters, distribution, and ecological preferences.

Material & methods

The material was examined using Nikon SMZ745 and Olympus SZ61 dissecting microscopes and an Olympus BX51 compound microscope. Tissues were examined and measured in water. Voucher specimens are deposited in the herbarium of V.L. Komarov Botanical Institute of RAS, Saint Petersburg, Russia (LE) and the Scientific Herbarium of Belarusian Polesie of Francisk Skorina Gomel State University, Gomel, Belarus (GSU). Duplicate specimens are stored in the Herbarium of the Institute of Experimental Botany of the National Academy of Sciences of Belarus, Minsk, Belarus (MSK). Nomenclature follows Lado (2019).

Taxonomy

Badhamia versicolor Lister, J. Bot. 39: 81. 1901.

FIG. 1

Mainly clustered, grey to dingy white, rugulose, sessile sporocarps with a narrowed base, 0.3–0.5 mm diam. Capillitium white. Spores ovoid, dull purple, minutely warted, 10–14 × 9–11 µm, arranged in spherical or elliptic clusters (frequently hollow) with 10–40 spores in each cluster. Plasmodium colourless.

SPECIMEN EXAMINED – BELARUS. MINSK REGION, Miadzel district, close to Konstantinovo village, 54°56'35"N 26°26'48"E, black alder forest, on wood of *Alnus glutinosa* (L.) Gaertn. (Betulaceae); 20.VIII.1995, E. Moroz (LE 320679, MSK-F 42108).

ECOLOGY & DISTRIBUTION. *Badhamia versicolor* is a facultatively corticolous species usually found in forest communities in temperate zone, although it can also thrive in arid areas (Abdel-Azeem & Salem Fatma 2013, Estrada-Torres & al. 2009, Wellman 2015). The bark of living trees, mosses, and lichens are the typical substrates (Pliszko & Bochynek 2017).

The species is known from all continents except Antarctica (Abdel-Azeem & Salem Fatma 2013, Macbride 1922, Moreno & al. 2013, Pliszko & Bochynek 2017, Ranade & al. 2012; Wellman 2015). In Europe *B. versicolor* has been reported from France, Germany, Great Britain, Italy, Poland, Russia (Leningrad region and the Republic of Karelia), Spain, Switzerland, Turkey, and Ukraine (Krzemieniewska 1960; Lado 1994; Martin & Alexopoulos 1969; Novozhilov 1993, 2005).

Despite its cosmopolitan range, *B. versicolor* is uncommon and often considered a rare species (Ing, 1999, Martin & Alexopoulos 1969). In Poland, *B. versicolor* is known as one of the rarest slime mould species, reported from only two localities (Pliszko & Bochynek 2017). Currently it is included in Polish national red list of myxomycetes (Drozdowicz & al. 2006).

In Belarus, the species was found within Narochansky National Park at the border of Blue Lakes landscape wildlife sanctuary, one of the most

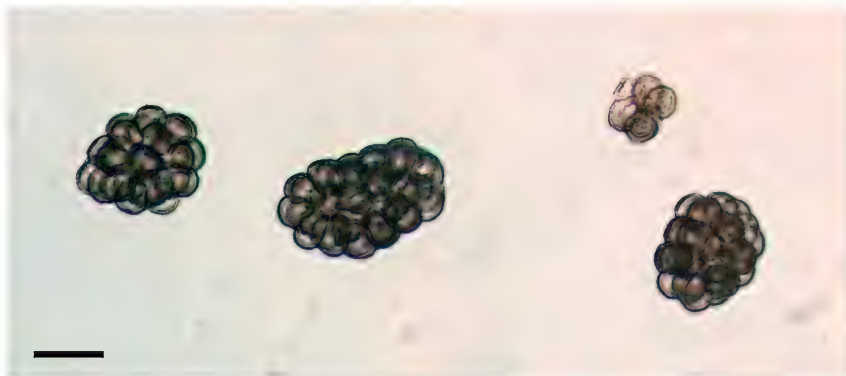


FIG. 1. *Badhamia versicolor* (LE 320679): spore clusters. Scale bar = 20 μ m.

undisturbed areas in the country. The forest area is dominated by *Alnus glutinosa* (black alder) with a high degree of waterlogging.

DISCUSSION. The most similar species are *B. capsulifera* (Bull.) Berk. and *B. dubia* Nann.-Bremek., which differ from *Badhamia versicolor* by smaller spore clusters and larger sporocarps (Pliszko & Bochynek 2017, Poulain & al. 2011). Our Belarusian voucher has a white capillitium and therefore resembles *B. papaveracea* Berk. & Ravenel, which differs by having stalked sporocarps (Poulain & al. 2011).

Trichia subfusca Rex, Proc. Acad. Nat. Sci. Philadelphia 42: 192. 1890.

FIG. 2

SPOROCARPS are scattered stalked sporangia, total height 0.8–1.5 mm. Sporotheca subglobose, brown, 0.4–0.8 mm diam. Stipe dark brown, reaching about half the sporocarp height. Peridium double, with an inner membranous and an outer cartilaginous layer. Dehiscence occurring at the top of the sporotheca. Capillitium formed by yellow elaters of 4.5–5.5 μ m diam. with 3–4 smooth spirals and with free, short, acute, rarely curved ends. Spores yellow in mass, pale yellow by transmitted light, 11–15 μ m diam., regularly warted. Plasmodium not seen.

SPECIMEN EXAMINED – BELARUS. GOMEL REGION, Buda-Koshelevo district, close to Rudnja-Olhovka village, 52°32'N 30°22'E, Scots pine forest, on thallus of lichen *Cladonia uncialis*, 7.VII.2005, A. Tsuryskau (GSU 00266, MSK-F 42461).

ECOLOGY AND DISTRIBUTION. Like other *Trichia* species, *T. subfusca* inhabits decaying wood (Schirmer & al. 2015).

Trichia subfusca is a very rare species (e.g., Schirmer & al. 2015), occasionally reported from Europe (Austria, Italy, Poland, Russia [Moscow



FIG. 2. *Trichia subfusca* (GSU 00266): capillitium and spores. Scale bar = 10 μ m.

and Murmansk regions, Perm Territory, Republic of Karelia, and Komi Republic], Spain, Sweden), Asia (India, Japan, Kazakhstan, Russia, Sri Lanka), and North America (Canada, USA) (Fefelov 2005; Gmoshinskiy 2014; Lado 1994; Novozhilov 1993, 2005; Schirmer & al. 2015; Vasyagina & al. 1977).

In Belarus the species was found in well-lit dry *Pinus sylvestris* L. (Scots pine) forest at the border of a sand quarry. The sporocarps were found on the terricolous lichen *Cladonia uncialis* (L.) F.H. Wigg. infected with lichenicolous fungus *Taeniolella beschiana* Diederich.

DISCUSSION. The *Trichia botrytis* group includes five morphologically related species: *T. botrytis* (J.F. Gmel.) Pers., *T. erecta* Rex, *T. flavicoma* (Lister) Ing, *T. munda* (Lister) Meyl., and *T. subfusca* (Schirmer & al. 2015). The species most similar to *T. subfusca* is *T. botrytis*, which differs in larger (2–3 mm.), areolate sporocarps with paler lines of dehiscence, elaters that gradually taper to long slender points, and smaller (9–11 mm.) spores. Also similar to *T. subfusca* is *T. macrospora* B. Zhang & Yu Li, distinguished by thicker (5–6 μ m diam.) elaters and larger (17–19 μ m diam.) densely verrucose spores (Zhang & Li 2016).

Acknowledgments

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***Vanderbylia cinnamomea* sp. nov. from southwestern China**

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ABSTRACT—*Vanderbylia cinnamomea* is proposed as a new wood-inhabiting polypore species based on morphological characters supported by phylogenetic analysis. The species is characterized by an annual, pileate basidiocarp, a brown to black pileal surface, an olivaceous buff to smoke grey pore surface, a dimitic hyphal system with clamped generative hyphae, and subglobose to amygdaliform, hyaline, thick-walled, smooth, dextrinoid, and cyanophilous basidiospores. ITS+nLSU sequence analyses place *V. cinnamomea* in *Vanderbylia* within a subclade with a high support (100% BS, 100% BP, 1.00 BPP) sister to a subclade comprising *V. fraxinea* and *V. robiniphila*.

KEY WORDS—*Perenniporia*, *Polyporaceae*, *Polyporales*, taxonomy, Yunnan Province

Introduction

Vanderbylia D.A. Reid (*Polyporaceae*, *Polyporales*) is typified by *V. vicina* (Lloyd) D.A. Reid (Reid 1973). Ryvarden & Johansen (1980) reduced the genus to a synonym under *Perenniporia* Murrill for a long time, but recent phylogenetic research of a combined sequence dataset of the internal transcribed spacer (ITS) and the large subunit nuclear ribosomal RNA gene (nLSU) supports *Vanderbylia* as an independent genus (Robledo &

al. 2009, Zhao & al. 2013, Cui & al. 2019). Morphologically *Vanderbylia* is characterized by pileate basidiocarps, a dimitic hyphal system with clamped generative hyphae and variably dextrinoid skeletal hyphae, and subglobose to amygdaliform, non-truncate and variably dextrinoid basidiospores (Reid 1973, Zhao & Cui 2013). Currently, nine species are accepted in *Vanderbylia* worldwide: *V. borneensis* Corner, *V. delavayi* (Pat.) B.K. Cui & Y.C. Dai, *V. devians* (Bres.) D.A. Reid, *V. fraxinea* (Bull.) D.A. Reid, *V. nigroapplanata* (Van der Byl) D.A. Reid, *V. robiniohila* (Murrill) B.K. Cui & Y.C. Dai, *V. subincarnata* Corner, *V. unguata* D.A. Reid, and *V. vicina* (Bresadola 1920, Reid 1975, Corner 1987, Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Ryvarden & Melo 2014, Cui & al. 2019).

Robledo & al. (2009), who revealed the relationship between *Perenniporia* and *Perenniporiella* Decock & Ryvarden, grouped two *Vanderbylia* species together—the generic type *V. vicina* and *V. fraxinea*. In their phylogenetic overview of *Perenniporia* s.l., Zhao & al. (2013) and revealed that *Vanderbylia fraxinea*, *V. robiniohila*, and *V. vicina* form a single lineage. Subsequently, Cui & al. (2019) investigated the species diversity, taxonomy, and phylogeny of *Polyporaceae* in China and proposed two new combinations, *Vanderbylia delavayi* and *V. robiniohila*.

During investigations on wood-inhabiting fungi in Yunnan Province, an additional taxon was found that could not be assigned to any described species. In examining the taxonomy and phylogeny of this new species, we employed a two-gene molecular phylogenetic approach using internal transcribed spacer (ITS) and long subunit (nLSU) plus an expanded sampling of *Vanderbylia* isolates that support the existence of a new species, *Vanderbylia cinnamomea*.

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, P.R. China (SWFC). Macromorphological descriptions are based on field notes. Color terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under light microscopy following Dai (2012). The following abbreviations are used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both non-amyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

We extracted genomic DNA from dried specimens using Magen Biotech HiPure Fungal DNA Mini Kit II according to the manufacturer's instructions with some

TABLE 1. Species, specimens, and sequences used in this study.
(New sequences in **bold**).

SPECIES NAME	SAMPLE NO.	GENBANK NO.		REFERENCES
		ITS	nLSU	
<i>Donkioporia expansa</i>	MUCL 35116	FJ411104	FJ393872	Robledo & al. (2009)
<i>Pyrofomes demidoffii</i>	MUCL 41034	FJ411105	FJ393873	Robledo & al. (2009)
<i>Vanderbylia cinnamomea</i>	CLZhao 8952 T	MT372778	MT372788	Present study
	CLZhao 8959	MT372779	MT372789	Present study
	CLZhao 8961	MT372780	MT372790	Present study
	CLZhao 8962	MT372781	MT372791	Present study
	CLZhao 8963	MT372782	MT372792	Present study
	CLZhao 9001	MT372783	MT372793	Present study
<i>V. fraxinea</i>	DP 83	AM269789	AM269853	Robledo & al. (2009)
	Cui 7154	HQ654095	HQ654110	Zhao & al. (2013)
	Cui 8871	JF706329	JF706345	Zhao & al. (2013)
<i>V. robinioiphila</i>	Cui 5644	HQ876609	JF706342	Zhao & al. (2013)
	Cui 7144	HQ876608	JF706341	Zhao & al. (2013)
	Cui 9174	HQ876610	JF706343	Zhao & al. (2013)
<i>V. vicina</i>	MUCL 44779	FJ411095	AF518666	Robledo & al. (2009)

modifications. A small piece (about 30 mg) of dried fungal material was ground to powder with liquid nitrogen, transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min. After the addition of 0.4 mL phenol-chloroform (24:1) to each tube, the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with 0.45 mL binding buffer. That mixture was transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 30 s. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 0.1 mL elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The ITS region was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi). The PCR procedure for ITS was optimized as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR condition for nLSU was as follow: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. The six new sequences from specimens of *Vanderbylia cinnamomea* were aligned with additional *Vanderbylia* sequences downloaded from GenBank (TABLE 1).

Sequences were aligned in MAFFT 7 (<http://mafft.cbrc.jp/alignment/server/>) using the “G-INS-I” strategy, and manually adjusted in BioEdit (Hall 1999).

Alignment datasets were deposited in TreeBase (submission ID 24081). GenBank sequences of *Donkioporia expansa* (Desm.) Kotl. & Pouzar and *Pyrofores demidoffii* (Lév.) Kotl. & Pouzar obtained from GenBank were used as an outgroup to root trees following Zhao & al. (2013) in the ITS+nLSU analysis.

Maximum parsimony analysis was applied to the ITS+nLSU dataset sequences. The tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BP) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Maximum Likelihood (ML) analysis with RAxML-HP2 was conducted for ITS datasets on Abe through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicate.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 2 million generations and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for greater than or equal to 80% (maximum likelihood, BL), 50% (maximum parsimony, BP), and 0.95 (Bayesian posterior probabilities, BPP) were considered as significantly supported.

Phylogenetic results

The ITS dataset included sequences from 15 fungal specimens or isolates representing 6 species. The dataset had an aligned length of 1844 characters, of which 1690 characters were constant, 65 were variable and parsimony-uninformative, and 89 were parsimony-informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 178, CI = 0.921, HI = 0.787, RI = 0.944, RC = 0.870). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian and ML analyses produced a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.001512 (BI).

The phylogeny (FIG. 1) inferred from ITS+nLSU sequences obtained for related taxa of *Vanderbylia* support the new species as independent in one sub-clade and sister to the /*fraxinea-robinophila* subclade.

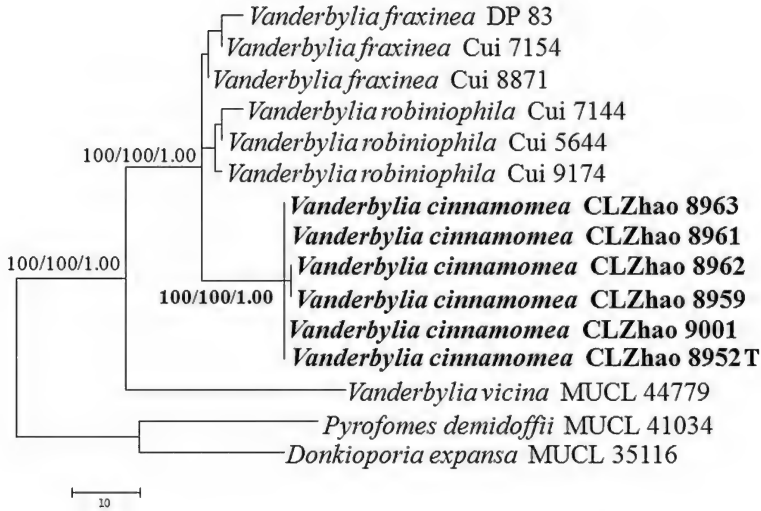


FIG. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Vanderbylia cinnamomea* and related species in *Vanderbylia* based on ITS+nLSU sequence analyses. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.

Taxonomy

Vanderbylia cinnamomea C.L. Zhao, sp. nov.

FIGS 2–4

MB 831788

Differs from *Vanderbylia vicina* by its annual basidiocarps and its smaller basidiospores.

TYPE: China. Yunnan Province: Kunming, Tanhuasi Park, on living tree of *Cinnamomum camphora* (L.) J. Presl (*Lauraceae*), 13 October 2018, CL Zhao 8952 (Holotype, SWFC 008952; GenBank MT372778, MT372788).

ETYMOLOGY: The specific epithet *cinnamomea* (Lat.) refers to the host of *Cinnamomum camphora*.

BASIDIOMATA annual, pileate, imbricate, without odor or taste and corky when fresh, becoming hard corky upon drying. Pilei dimidiate, projecting ≤10 cm, 18 cm wide, 4.5 cm thick at centre. Pileal surface pale brown to brown when fresh and brown to black from the base upon drying, smooth, gently concentrically sulcate, glabrous. Pore surface pure buff to olivaceous buff when fresh, olivaceous buff to smoke grey upon drying; pores round, 5–7 per mm; dissepiments thick, entire. Sterile margin narrow, buff, ≤0.5

mm wide. Context cream, cottony, ≤ 4 cm thick. Tubes concolorous with pore surface, ≤ 5 mm long.

HYPHAL STRUCTURE dimitic; generative hyphae with clamp connections, strongly dextrinoid, CB+; tissues unchanging in KOH.

CONTEXT generative hyphae infrequent, hyaline, thin-walled, unbranched, 2–3 μm in diam; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, branched, interwoven, 4.5–5.5 μm in diam.

TUBES generative hyphae infrequent, hyaline, thin-walled, unbranched, 1.5–2.5 μm in diam; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, branched, interwoven, 4–5 μm in diam. Presence of arboriform hyphae, thick-walled to almost solid, with few branches and short, lateral or terminal processes, tortuous, $25\text{--}40 \times 2\text{--}6 \mu\text{m}$. Cystidia and cystidioles not seen; basidia clavate, with 4 sterigmata and a basal clamp connection, $20\text{--}24 \times 6\text{--}9.5 \mu\text{m}$; basidioles dominant, clavate-shaped to pear-shaped.

BASIDIOSPORES subglobose to amygdaliform, hyaline, thick-walled, smooth, strongly dextrinoid, cyanophilous, $5\text{--}6(-6.5) \times 4\text{--}5(-5.5) \mu\text{m}$, $L = 5.67 \mu\text{m}$, $W = 4.73 \mu\text{m}$, $Q = 1.17\text{--}1.21$ ($n = 180/6$).

TYPE OF ROT: white.

ADDITIONAL SPECIMENS EXAMINED: CHINA. YUNNAN PROVINCE. Kunming: Tanhuasi Park, on living tree of *Cinnamomum camphora*, 15 October 2018, CLZhao 8959 (SWFC 008959; GenBank MT372779, MT372789); CLZhao 8961 (SWFC 008961; GenBank MT372780, MT372790); CLZhao 8962 (SWFC 008962, GenBank MT372781, MT372791); CLZhao 8963 (SWFC 008963; GenBank MT372782, MT372792); CLZhao 9001 (SWFC 009001; GenBank MT372783, MT372793).

Discussion

We describe here a new species *Vanderbylia cinnamomea* based on phylogenetic analyses and morphological characters.

Phylogenetically, *Vanderbylia cinnamomea* grouped with species *V. fraxinea*, *V. robiniophila*, and *V. vicina* in the rDNA-based phylogeny (FIG. 1). Morphologically *V. fraxinea* differs in its perennial basidiocarps and larger basidiospores ($6\text{--}8 \times 5\text{--}6.5 \mu\text{m}$, Ryvarden & Melo 2014), while *Vanderbylia robiniophila* is distinguished by its growth on *Robinia* L., its white to pale brown pore surface, and its larger basidiospores ($5\text{--}8 \times 5\text{--}7 \mu\text{m}$, Gilbertson & Ryvarden 1987; Núñez & Ryvarden 2001); *Vanderbylia vicina* differs in its perennial basidiocarps and larger basidiospores ($8\text{--}8.9 \times 6.9\text{--}7.5 \mu\text{m}$, Reid 1973).

Four species are morphologically similar to *Vanderbylia cinnamomea*: *V. borneensis*, *V. devians*, *V. subincarnata*, and *V. unguolata*. *Vanderbylia*

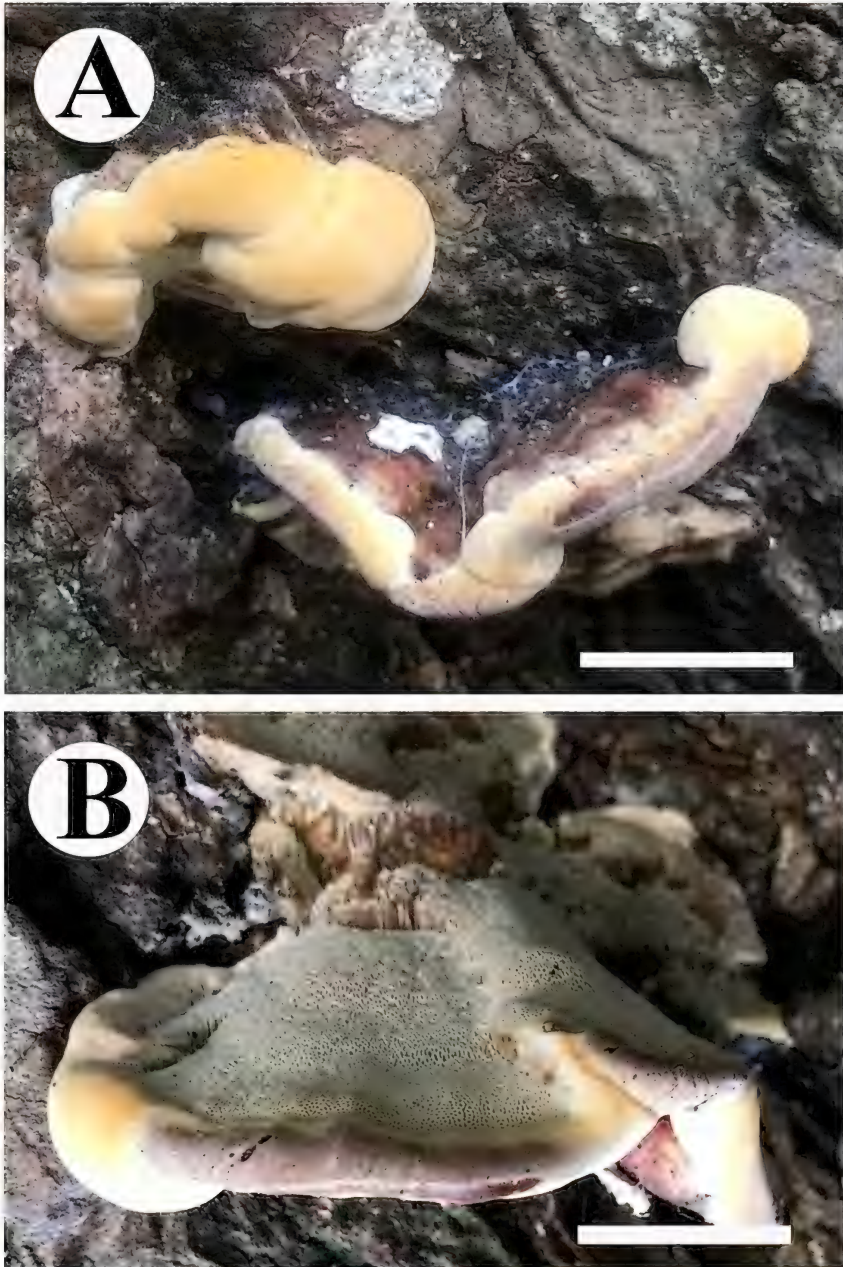


FIG. 2. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
Basidiocarps. Scale bars = 5 cm.

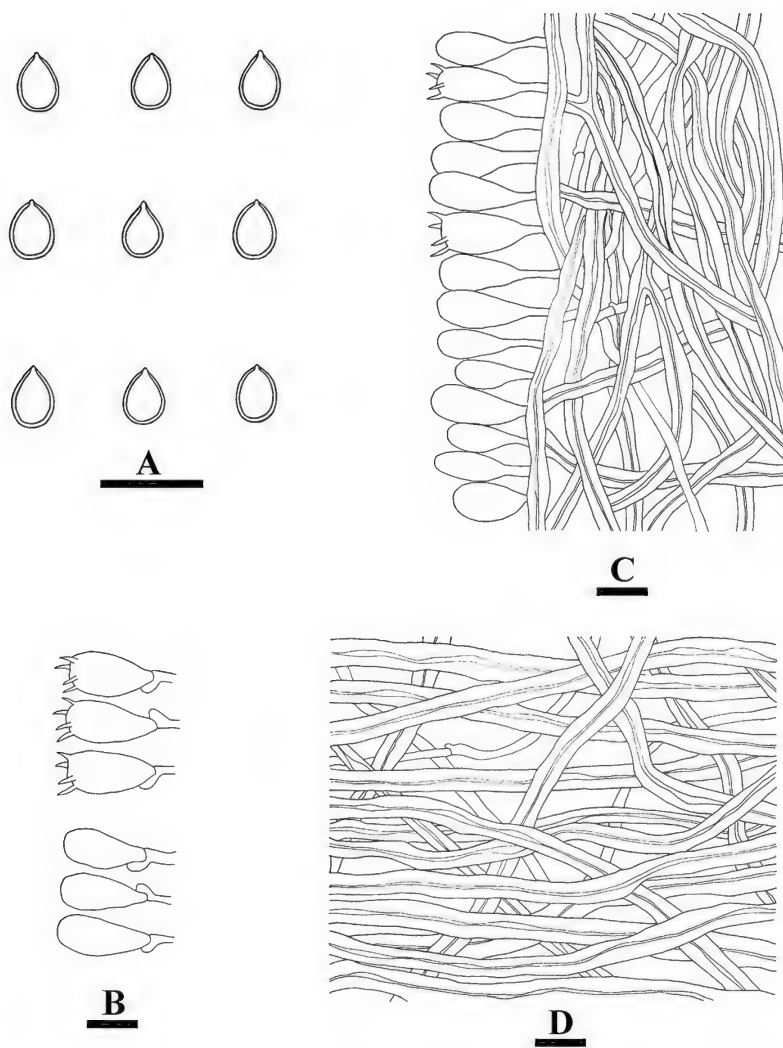


FIG. 3. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
A. Basidiospores; B. Basidia and basidioles; C. Hyphae from trama; D. Hyphae from context.
Scale bars = 10 μ m.

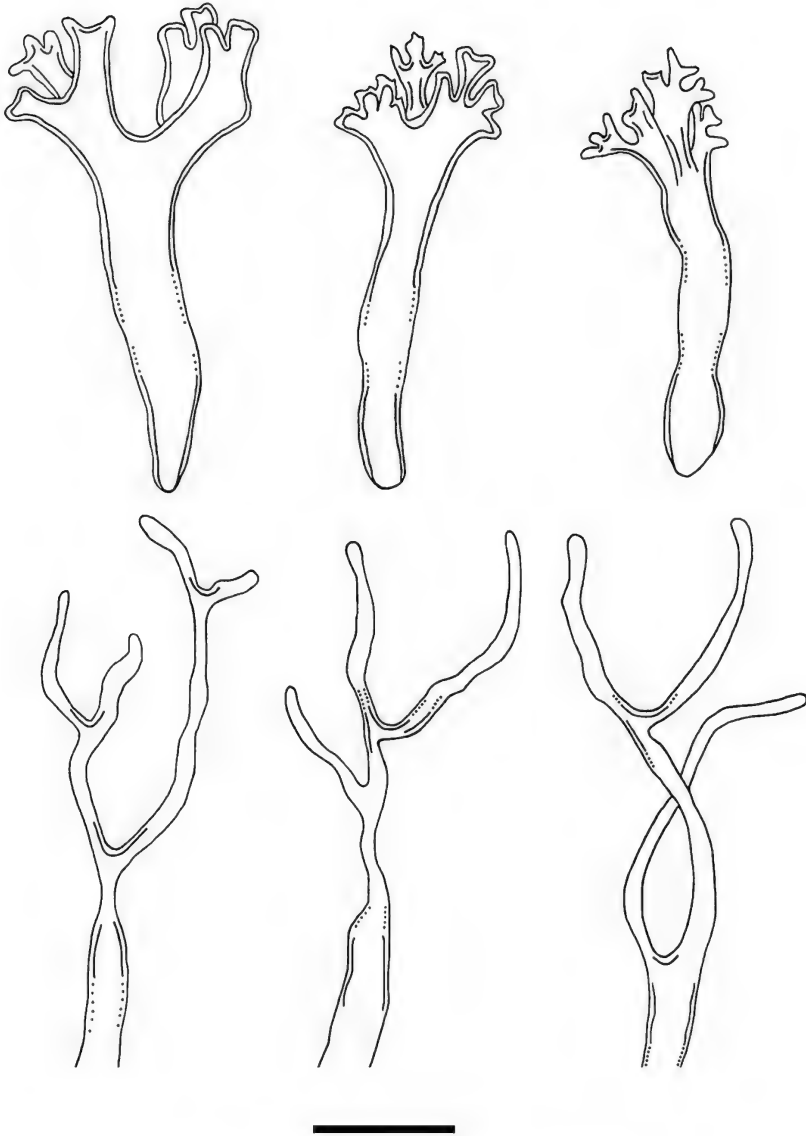


FIG. 4. *Vanderbylia cinnamomea* (holotype, SWFC 008952).
Arboriform hyphae. Scale bar = 10 μ m.

borneensis differs from *V. cinnamomea* in its smaller pores (8–10 per mm) and the presence of skeletal hyphal endings in the dissepiments (Corner 1987); *V. devians* is distinguished by its substipitate basidiocarps with alutaceous to isabelline pore surface and larger pores (3–4 per mm, Bresadola 1920); *V. subincarnata* is diagnosed by its pinkish pore surface and smaller pores (7–10 per mm, Corner 1987); and *V. unguolata* has unguulate basidiocarps with an ochraceous pore surface and hyaline to yellow basidiospores (Ryvarden & Johansen 1980).

When Decock & Ryvarden (1999) examined the holotype of *Polyporus delavayi* Pat., they proposed that it be transferred to *Perenniporia* based on its strongly dextrinoid, cyanophilous skeletal hyphae and dextrinoid, thick-walled basidiospores; they also examined the type specimen of *Perenniporia formosana* T.T. Chang and synonymized it under *P. delavayi* (Pat.) Decock & Ryvarden. Cui & al. (2019) subsequently transferred *Polyporus delavayi* to *Vanderbylia* based on molecular data and morphological characters on finding *P. delavayi* nested within the *Vanderbylia* lineage and manifesting morphological features consistent with the concept of *Vanderbylia*. Morphologically, *V. delavayi* differs from *V. cinnamomea* by its dirty greyish orange to greyish brown pore surface, larger pores (4–5 per mm), and larger basidiospores ($5.7\text{--}7 \times 4.7\text{--}5.9 \mu\text{m}$, Decock & Ryvarden 1999).

Wood-rotting basidiomycetes have been extensively studied (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014), but Chinese wood-rotting fungi diversity is still not well known, especially in the subtropics and tropics. The new species *Vanderbylia cinnamomea* is from the Chinese subtropics, where many new taxa in *Polyporales* have been described (Cui & al. 2007, 2011; Cui & Dai 2008; Du & Cui 2009; Li & Cui 2010; He & Li 2011; Jia & Cui 2011; Yu & al. 2013; Yang & He 2014; Chen & al. 2015; Zhao & Wu 2017; Shen & al. 2018; Zhao & Ma 2019). We anticipate that more new polypore taxa will be found in China after further investigations and molecular analyses.

Acknowledgments

Special thanks are due to Drs. Shah Hussain (University of Swat, Pakistan) and Yuan-Yuan Chen (Henan Agricultural University, P.R. China) who reviewed the manuscript. The research was supported by the National Natural Science Foundation of China (Project No. 31700023) and the Science Foundation of Yunnan Department of Education (2018JS326) and the Key Laboratory of State Forestry Administration for Highly Efficient Utilization of Forestry Biomass Resources in Southwest China (Southwest Forestry University) (Project No. 2019-KF10).

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G.H. Cunningham’s use of te reo Māori in fungal epithets

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ABSTRACT—New Zealand mycologist G.H. Cunningham (1892–1962) frequently used the indigenous language of New Zealand, te reo Māori, when creating epithets for new species and replacement names. All of these epithets are listed, and nomenclatural treatments (including etymologies) of the taxa are presented. In addition, tables cite all te reo Māori and te reo-derived generic names and epithets published by mycological authors. Guidelines are discussed for the appropriate orthography for names and epithets derived from te reo Māori and other non-latin vernacular languages.

KEY WORDS—ta reo Māori, undeclinable epithets, nouns in apposition, diacritical marks, host species

Introduction

Gordon Herriot Cunningham (1892–1962), who was New Zealand’s first resident professional mycologist (McKenzie 2004; <https://teara.govt.nz/en/biographies/4c47/cunningham-gordon-herriot>), is regarded as the “Father of New Zealand Plant Pathology and Mycology.” After about 17 years of employment in the Department of Agriculture, during which he gained B.Sc., M.Sc., and Ph.D. degrees, Cunningham served the Department of Scientific and Industrial Research [DSIR] as Director of the Plant Diseases Division [PDD] from its foundation in 1936 until his death; his numerous dried specimens formed the foundation of the current New Zealand Fungarium (PDD). His initial focus was mainly on plant pathology, but taxonomic mycology soon became a passion, and he published numerous papers and monographic books on rust fungi, gasteromycetes, polypores, and thelephoraceous fungi.

A feature of Cunningham's new taxa was his frequent use of fungal epithets drawn from te reo Māori [the indigenous language of Aotearoa/New Zealand] (Pennycook & McKenzie 2002). A survey across all biological disciplines (Veale & al. 2019) identified Cunningham as the fourth most prolific proponent of this practice (after an arachnologist and two malacologists) but did not discuss his contribution. A search of Cunningham's taxonomic publications has identified 56 species (proposed as either sp. nov. or nom. nov.) with 49 epithets either drawn directly, or derived, from te reo Māori. These are presented here, with nomenclatural, taxonomic, and etymological details. In addition, tables are presented of te reo Māori and te reo-derived genus names and species/subspecies/variety epithets published by all mycological authors. Guidelines are discussed for the appropriate orthography for names and epithets derived from te reo Māori and other non-latinate vernacular languages.

Materials & methods

All of Cunningham's taxonomic publications were searched; 22 of them proposed names with te reo Māori or te reo-derived epithets (Cunningham 1923, 1924a,b, 1928, 1930, 1931, 1938, 1944, 1945a,b, 1947, 1948a,b,c, 1949, 1953a,b, 1954, 1955, 1956, 1963, 1965).

For a comprehensive overview of te reo Māori or te reo-derived fungal names (genera, species, subspecies, and varieties), a careful search was made of comprehensive modern listings of New Zealand fungi (Buchanan & Ryvarden 2000; Gadgil & al. 2005; Galloway 2007; Gordon 2012; Horak 2008, 2018; Pennycook 1989, 2004; Pennycook & Galloway 2004; Petersen 1988; Stephenson 2003; Vánky & McKenzie 2002), and these were cross-checked and augmented by searches of the major mycological nomenclature websites (Index Fungorum 2020, MycoBank 2020, Ngā Harore 2020). Epithets derived from other Polynesian languages (e.g., Hawai'ian, Tahitian) and epithets with a misleading similarity to te reo Māori (e.g., *wainioi* referring to the Finnish lichenologist Vainio/Wainio; *waikerieanum* from the Australian locality Waikerie) were deleted from the search results.

Cunningham's epithets

The 49 te reo Māori or te reo-derived fungal epithets proposed by Cunningham are listed alphabetically. Presented beneath each epithet are the new species or replacement names in which the epithet was first published, together with all subsequent homotypic synonyms in which the epithet was recombined. The currently accepted name for each species is indicated with bold font. The etymology of each epithet is explained, together with the type host and the type locality when these are relevant to the etymology; in addition, the host species of the type specimen is listed for all rust species, even if not involved in the etymology. Māori names of host plants were sourced from Williams (1971) and Beever (1991). Localities are referred to the "Crosby

districts” defined by Crosby & al. (1998). Host nomenclature and synonymy follows Ngā Tipu (2020).

akiraho

Puccinia akiraho G. Cunn., Trans. & Proc. New Zealand Inst. 61: 411. 1930.

≡ *Puccinia novae-zelandiae* G. Cunn., Trans. & Proc. New Zealand

Inst. 54: 686. 1923. [non *P. novozelandica* Bubak 1901].

TYPE HOST: *Olearia forsteri* (*Compositae*) [= *Olearia paniculata* (J.R. Forst. & G. Forst.) Druce].

ETYMOLOGY: **akiraho**, Māori name for *Olearia paniculata*.

aorangi

Puccinia aorangi G. Cunn., Trans. & Proc. New Zealand Inst. 61: 411. 1930.

TYPE LOCALITY & HOST: 1600–2000 m altitude on Taranaki/Mt Egmont, North Island; *Celmisia major* Cheeseman (*Compositae*) [= *Celmisia major* var. *brevis* Allan, the variety endemic to Taranaki/Mt Egmont].

ETYMOLOGY: **aorangi/aoraki** [“cloud-piercer”], Māori name (and common name) for Mt Cook, South Island; perhaps used in a general sense, referring to the type locality on a North Island cloud-piercer.

= *Puccinia egmontensis* G. Cunn., Trans. & Proc. New Zealand Inst. 54: 681. 1923.

aotearoa

Lachnella aotearoa G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 145: 331. 1963.

≡ *Flagelloscypha aotearoa* (G. Cunn.) Agerer, Mitt.

Bot. Staatssamml. München 19: 252. 1983

ETYMOLOGY: **aotearoa**, Māori name (and common name) for New Zealand.

Stereum aotearoa G. Cunn., Trans. Roy. Soc. New Zealand 84(2): 212. 1956.

ETYMOLOGY: **aotearoa**, Māori name (and common name) for New Zealand.

aroa

Poria aroa G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 72: 39. 1947.

≡ *Flaviporus aroa* (G. Cunn.) G. Cunn., New Zealand

Dept. Sci. Industr. Res., Bull. 164: 150. 1965.

ETYMOLOGY: **aroa**, Māori, referring to the type locality, Mt Te Aroha, Bay of Plenty.

= *Australoporus tasmanicus* (Berk.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 5. 1988.

awhitu

Fomes awhitu G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 79: 16. 1948.

ETYMOLOGY: **āwhitu**, Māori, referring to the type locality, Awhitu Peninsula, Auckland.

= *Abundisporus roseoalbus* (Jung.) Ryvarden, Belg. J. Bot. 131: 154. 1999.

haumata

Uredo haumata G. Cunn., Trans. & Proc. New Zealand Inst. 59: 499. 1928.

Correct name will combine this epithet in *Uromyces* (E.H.C. McKenzie, in prep.).

TYPE HOST: *Danthonia cunninghamii* (Gramineae) [= *Chionochloa conspicua* subsp. *cunninghamii* (Hook.f.) Zotov].

ETYMOLOGY: **haumata**, Māori name for broad-leaved snowgrass, *Chionochloa* spp.

= *Uromyces macnabbii* Cummins, Rust Fungi Cereals, Grasses and Bamboos: 483. 1971.

hautu

“*Hysterangium hautu*” G. Cunn., Trans. & Proc. Roy. Soc. New Zealand 67: 409. 1938, nom. inval. [no Latin description].

≡ *Protuberia hautuensis* Castellano & Beever, New Zealand J. Bot. 32: 322. 1994.

ETYMOLOGY: **hautū**, Māori name for the type locality, Waimarino, Taupo.

heketara

Puccinia heketara G. Cunn., Trans. & Proc. New Zealand Inst. 55: 393. 1924.

TYPE HOST: *Olearia cunninghamii* (Compositae) [= *Olearia rani* (A. Cunn.) Druce].

ETYMOLOGY: **heketara**, Māori name for *Olearia rani*.

= *Puccinia atkinsonii* G. Cunn., Trans. & Proc. New Zealand Inst. 54: 675. 1923.

hoheriae

Puccinia hoheriae G. Cunn., Trans. & Proc. New Zealand Inst. 54: 661. 1923, nom. illeg. [non Wakefield 1917].

TYPE HOST: *Hoheria populnea* A. Cunn. (Malvaceae).

ETYMOLOGY: genitive case of generic name (and common name) *Hoheria*, derived from **hōhere**, Māori name for *Hoheria* spp.

= *Puccinia hoheriae* Wakef., Bull. Misc. Inform. Kew. 1917: 312. 1917.

= *Puccinia plagianthi* McAlpine, Proc. Roy. Soc. Victoria 7: 218. 1895.

horopito

Uredo horopito G. Cunn., Trans. & Proc. Roy. Soc. New Zealand 75: 326. 1945.

TYPE HOST: *Pseudowintera axillaris* (J.R. Forst. & G. Forst.) Dandy (Winteraceae).

ETYMOLOGY: **horopito**, Māori name (and common name) for *Pseudowintera* spp.

huia

Solenia huia G. Cunn., Trans. Roy. Soc. New Zealand 81(2): 179. 1953.

≡ *Porothelium huia* (G. Cunn.) W.B. Cooke, Mycologia 49: 691. 1957.

≡ *Stigmatolemma huia* (G. Cunn.) W.B. Cooke, Beih. Sydowia 4: 128. 1961.

≡ *Stromatoscypha huia* (G. Cunn.) G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 145: 305. 1963.

≡ *Resupinatus huia* (G. Cunn.) Thorn & al., Mycologia 97: 1148. 2006.

ETYMOLOGY: **huia**, Māori, referring to the type locality, Huia, Auckland.

hunua

Poria hunua G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div.,
Bull. 72: 39. 1947.

≡ *Antrodiella hunua* (G. Cunn.) Ryvarden, Prelim. Polyp. Fl. E. Africa: 257. 1980.

≡ *Flaviporus hunua* [as “*hunuus*”] (G. Cunn.) Ginns, Mycotaxon 21: 326. 1984.

ETYMOLOGY: *hūnua*, Māori, referring to the type locality, Hunua Range, Auckland.

hupiro

Aecidium hupiro G. Cunn., Trans. & Proc. New Zealand Inst. 55: 36. 1924.

TYPE HOST: *Coprosma foetidissima* J.R. Forst. & G. Forst. (*Rubiaceae*).

ETYMOLOGY: *hūpiro*, Māori name for *Coprosma foetidissima*.

kaiku

Caecoma kaiku G. Cunn., Trans. & Proc. New Zealand Inst. 61: 416. 1930.

TYPE HOST: *Parsonsia capsularis* (G. Forst.) DC. × *heterophylla* A. Cunn.
(*Apocynaceae*).

ETYMOLOGY: *kaikū*, Māori name for *Parsonsia* spp.

kamahi

Fuscoporia kamahi G. Cunn., New Zealand Dept. Sci. Industr. Res.,
Bull. 164: 263. 1965.

≡ *Phellinus kamahi* (G. Cunn.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 15. 1988.

TYPE HOST: *Weinmannia racemosa* L.f. (*Cunoniaceae*).

ETYMOLOGY: *kāmahi*, Māori name (and common name) for *Weinmannia racemosa*.

karetu

Uredo karetu G. Cunn., Trans. & Proc. New Zealand Inst. 55: 41. 1924.

TYPE HOST: *Hierochloa redolens* (Vahl) Roem. & Schult. (*Gramineae*).

ETYMOLOGY: *kāretu*, Māori name (and common name) for *Hierochloa redolens*.

kauri

Corticium kauri G. Cunn., Trans. Roy. Soc. New Zealand 82: 303. 1954.

TYPE SUBSTRATE: much decayed wood of *Agathis australis* (D. Don) Lindl. ex
Loudon (*Araucariaceae*).

ETYMOLOGY: *kauri*, Māori name (and common name) for *Agathis australis*.

keae

Puccinia keae G. Cunn., Trans. & Proc. New Zealand Inst. 59: 493. 1928.

TYPE HOST: *Olearia nummulariifolia* (Hook.f.) Hook.f. (*Compositae*).

ETYMOLOGY: *kea*, Māori name (and common name) for *Nestor notabilis* [mountain
parrot]; referring to the type locality, Kea Point, Mackenzie.

koherika

Puccinia koherika G. Cunn., Trans. & Proc. New Zealand Inst. 61: 408. 1930.

TYPE HOST: *Angelica rosifolia* Hook. (*Umbelliferae*) [= *Scandia rosifolia* (Hook.) J.W. Dawson].

ETYMOLOGY: **koheriki**, Māori name for *Scandia rosifolia*.

konini

Uredo konini G. Cunn., Trans. & Proc. New Zealand Inst. 59: 502. 1928, nom. illeg.
[a superfluous nom. nov., proposed to avoid creating a comb. nov. that would be an illegitimate later homonym of *Uredo fuchsiae* Arthur & Holway 1918; however, Cunningham was apparently unaware that the combination had already been published legitimately in 1903].

≡ *Coleosporium fuchsiae* Cooke, Grevillea 14: 129. 1886

≡ *Uredo fuchsiae* (Cooke) Henn., Beibl. Hedwigia 42: (73). 1903.

TYPE HOST: *Fuchsia excorticata* (Vahl) Roem. & Schult. (*Onagraceae*).

ETYMOLOGY: **kōnini**, Māori name for fruit of *Fuchsia excorticata*.

= *Mikronegria fuchsiae* P.E. Crane & R.S. Petersen, New Zealand J. Bot. 45: 709. 2007.

kopoti

Puccinia kopoti G. Cunn., Trans. & Proc. New Zealand Inst. 54: 668. 1923.

TYPE HOST: *Anisotome aromatica* Hook.f. (*Umbelliferae*).

ETYMOLOGY: **kopoti**, Māori name for *Anisotome aromatica*.

kowhai

Aecidium kowhai G. Cunn., Trans. & Proc. New Zealand Inst. 55: 35. 1924.

TYPE HOST: *Edwardsia tetraptera* (*Leguminosae*) [= *Sophora tetraptera* J.F. Mill.].

ETYMOLOGY: **kōwhai**, Māori name (and common name) for *Sophora* spp.

= *Uromyces edwardsiae* G. Cunn., Trans. & Proc. New Zealand Inst. 55: 392. 1924.

maire

Laricifomes maire G. Cunn., New Zealand Dept. Sci. Industr. Res.,
Bull. 164: 262. 1965.

≡ *Fomitopsis maire* (G. Cunn.) P.K. Buchanan & Ryvarden,
Mycotaxon 31: 15. 1988.

TYPE HOST: *Gymnelaea cunninghamii* (*Oleaceae*) [= *Nestegis cunninghamii* (Hook.f.) L.A.S. Johnson].

ETYMOLOGY: **maire**, Māori name (and common name) for *Nestegis* spp.

mania

Puccinia mania G. Cunn., Trans. & Proc. New Zealand Inst. 61: 404. 1930.

TYPE HOST: *Carex wakatipu* Petrie (*Cyperaceae*).

ETYMOLOGY: **mānia**, Māori name for some *Carex* spp.

manuka

Poria manuka G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 72: 38. 1947.

≡ *Oligoporus manuka* (G. Cunn.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 17. 1988.

≡ *Postia manuka* (G. Cunn.) P.K. Buchanan & Ryvarden, New Zealand J. Bot. 38(2): 303. 2000.

TYPE HOST: *Leptospermum scoparium* J.R. Forst. & G. Forst. (*Myrtaceae*).

ETYMOLOGY: **mānuka**, Māori name (and common name) for *Leptospermum scoparium*.

maurea

Puccinia maurea G. Cunn., Trans. & Proc. New Zealand Inst. 61: 406. 1930.

TYPE HOST: *Carex inversa* R. Br. (*Cyperaceae*).

ETYMOLOGY: **maurea**, Māori name for some *Carex* spp.

namua

Puccinia namua G. Cunn., Trans. & Proc. New Zealand Inst. 55: 3. 1924.

TYPE HOST: *Anisotome filifolia* (Hook.f.) Cockayne & Laing (*Umbelliferae*).

ETYMOLOGY: **namua**, derivation unknown. (Similar te reo Māori words are *namu* for sandfly [blackfly] or mosquito; and *namunamu* for indigenous *Geranium* spp. and the exotic weed *Geranium molle* (*Geraniaceae*). The Māori name for *Anisotome aromatica* is **kopoti**.)

nikau

Epithele nikau G. Cunn., Trans. Roy. Soc. New Zealand 83: 629. 1956.

≡ *Skeletohydnum nikau* (G. Cunn.) Jülich, Persoonia 10: 331. 1979.

TYPE HOST: *Rhopalostylis sapida* H. Wendl. & Drude (*Palmae*).

ETYMOLOGY: **nikau**, Māori name (and common name) for *Rhopalostylis sapida*.

Lachnella nikau G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 145: 331. 1963.

TYPE HOST: *Rhopalostylis sapida* H. Wendl. & Drude (*Palmae*).

ETYMOLOGY: **nikau**, Māori name (and common name) for *Rhopalostylis sapida*.

Peniophora nikau G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 145: 127. 1963.

≡ *Peniophora sororia* G. Cunn., Trans Roy. Soc. New Zealand 83(2): 280. 1955, nom. illeg. [non Bourdot & Galzin 1913].

≡ *Subulicystidium nikau* (G. Cunn.) Jülich, Ber. Deutsch. Bot. Ges. 81(9): 419. 1969 ["1968"].

TYPE HOST: *Rhopalostylis sapida* H. Wendl. & Drude (*Palmae*).

ETYMOLOGY: **nikau**, Māori name (and common name) for *Rhopalostylis sapida*.

otagensis/-ense

Corticium otagense G. Cunn., New Zealand Dept. Sci. Industr. Res.,
Bull. 145: 331. 1963.

ETYMOLOGY: referring to the European name Otago (historically the southernmost province of New Zealand), derived from **ōtākou**, a Kāi Tahu [southern Māori] locality name [see also the **otakou** epithet entry, below]; the guttural Kāi Tahu pronunciation of 'k' was misheard as a 'g' by early settlers.

Pellicularia otagensis G. Cunn., Trans. Roy. Soc. New Zealand 81: 324. 1953.

≡ *Sistotrema otagense* (G. Cunn.) Stalpers & P.K.

Buchanan, New Zealand J. Bot. 29: 331. 1991.

ETYMOLOGY: referring to the European name Otago (historically the southernmost province of New Zealand), derived from **ōtākou**, a Kāi Tahu [southern Māori] locality name [see also the **otakou** epithet entry, below]; the guttural Kāi Tahu pronunciation of 'k' was misheard as a 'g' by early settlers.

otakou

Poria otakou G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div.,
Bull. 72: 38. 1947.

≡ *Ceriporia otakou* (G. Cunn.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 22. 1988.

≡ *Gloeoporus otakou* (G. Cunn.) Zmitr. & Spirin, Mycena 6: 35. 2006.

ETYMOLOGY: **ōtākou**, Māori name of the Kāi Tahu kaika [village] near Taiaroa Head, Otago Peninsula, where in 1848 Scottish settlers made their first contact with tangata whenua [the people of the land]; referring to the type locality, Kinloch, Otago Lakes.

Uromyces otakou G. Cunn., Trans. & Proc. New Zealand Inst. 54: 627. 1923.

TYPE HOST: *Poa caespitosa* Spreng. (*Gramineae*) [= *Poa cita* Edgar].

ETYMOLOGY: **ōtākou**, Māori name of the Kāi Tahu kaika [village] near Taiaroa Head, Otago Peninsula, where in 1848 Scottish settlers made their first contact with tangata whenua [the people of the land]; referring to the type locality, Routeburn Valley, Otago Lakes.

otira

Aecidium otira G. Cunn., Trans. & Proc. New Zealand Inst. 59: 498. 1928.

Correct name will combine this epithet in *Puccinia* (E.H.C. McKenzie, in prep.).

TYPE HOST: *Olearia arborescens* (G. Forst.) Cockayne & Laing (*Compositae*).

ETYMOLOGY: **ōtira**, Māori name for the Otira river flowing westward from the vicinity of the type locality, Arthurs Pass, North Canterbury.

pirongia

Poria pirongia G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div.,
Bull. 72: 39. 1947.

≡ *Haploporus pirongia* (G. Cunn.) Meng Zhou & al., MycoKeys 54: 92. 2019.

ETYMOLOGY: **p irongia**, Māori, referring to the type locality, Mt Pirongia, Waikato.

pounamu

Puccinia pounamu G. Cunn., Trans. & Proc. New Zealand Inst. 54: 688. 1923.

TYPE HOST: *Senecio southlandicus* (Compositae) [= *Brachyglottis lagopus* (Raoul) B. Nord.].

ETYMOLOGY: **pounamou**, Māori word for greenstone [nephrite jade]; referring to the type locality Greenstone Valley, Otago Lakes.

rata

Poria rata G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 72: 40. 1947.

≡ ***Antrodiella rata*** (G. Cunn.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 25. 1988.

TYPE HOST: *Metrosideros robusta* A. Cunn. (Myrtaceae).

ETYMOLOGY: **rātā**, Māori name (and common name) for some *Metrosideros* spp.

rautahi

Puccinia rautahi G. Cunn., Trans. & Proc. New Zealand Inst. 61: 405. 1930.

TYPE HOST: *Carex gaudichaudiana* Kunth (Cyperaceae).

ETYMOLOGY: **rautahi**, Māori name for some *Carex* spp.

tararua

Puccinia tararua G. Cunn., Trans. & Proc. New Zealand Inst. 54: 671. 1923.

TYPE HOST: *Gentiana patula* (Gentianaceae) [= *Gentianella patula* (Kirk) Holub].

ETYMOLOGY: **tararua**, Māori; referring to the type locality, Tararua Ranges, Wellington.

tawa

Trametes tawa G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 80: 9. 1948.

≡ ***Metuloidea tawa*** (G. Cunn.) G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 164: 250. 1965.

FREQUENT SUBSTRATE: bark of dead upright branches of *Beilschmiedia tawa* (A. Cunn.) Benth. & Hook.f. ex Kirk (Lauraceae).

ETYMOLOGY: **tawa**, Māori name (and common name) for *Beilschmiedia tawa*.

= ***Metuloidea rhinocephala*** (Berk.) Miettinen, Ann. Bot. Fenn. 53(3-4): 165. 2016.

tawhai

Fuscoporia tawhai G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div., Bull. 73: 8. 1948.

≡ ***Phellinus tawhai*** (G. Cunn.) G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 164: 229. 1965.

TYPE HOST: *Nothofagus cliffortioides* (Nothofagaceae) [= *Fuscospora cliffortioides* (Hook.f.) Heenan & Smissen].

ETYMOLOGY: **tāwhai/tāwai**, Māori name for *Nothofagus* [= *Fuscospora* and *Lophozonia*] spp.

tiritea

Puccinia tiritea G. Cunn., Trans. & Proc. New Zealand Inst. 54: 654. 1923.

TYPE HOST: *Muehlenbeckia australis* (G. Forst.) Meisn. (*Polygonaceae*).

ETYMOLOGY: **turitea/tiritea**, Māori; referring to the type locality, Turitea, Wellington.

= *Puccinia otagensis* (Linds.) McKenzie & Padamsee, Pl. Pathol. 66: 1252. 2017.

toa

Puccinia toa G. Cunn., Trans. & Proc. New Zealand Inst. 61: 408. 1930.

≡ *Puccinia haloragis* [as “*halorrhagidis*”] G. Cunn., Trans. & Proc. New Zealand Inst. 54: 664. 1923, nom. illeg. [non Sydow & Sydow 1913].

TYPE HOST: *Haloragis* [as “*Halorrhagis*”] *depressa* (*Haloragaceae*) [= *Gonocarpus aggregatus* (Buchanan) Orchard].

ETYMOLOGY: **toa/toatoa**, Māori name for some *Haloragis* spp.

toatoa

Tyromyces toatoa G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 164: 262. 1965.

TYPE HOST: *Phyllocladus alpinus* Hook.f. (*Podocarpaceae*).

ETYMOLOGY: **toatoa**, Māori name for *Phyllocladus* spp.

toetoe

Uredo toetoe G. Cunn., Trans. & Proc. New Zealand Inst. 55: 41. 1924.

TYPE HOST: *Arundo conspicua* (*Gramineae*) [≡ *Chionochloa conspicua* (G. Forst.) Zotov].

ETYMOLOGY: **toetoe**, Māori name (and common name) for *Chionochloa conspicua*.

tongariro

Cyphella tongariro G. Cunn., Trans. Roy. Soc. New Zealand 81: 185. 1953.

≡ *Lachnella tongariro* (G. Cunn.) W.B. Cooke, Beih. Sydowia 4: 80. 1961.

≡ *Flagelloscypha tongariro* (G. Cunn.) Agerer, Sydowia 32: 9. 1980 [“1979”].

ETYMOLOGY: **tongariro**, Māori; referring to the type locality, Mt Tongariro, Taupo.

totara

Cyphella totara G. Cunn., Trans. Roy. Soc. New Zealand 81: 182. 1953.

≡ *Calyptella totara* (G. Cunn.) W.B. Cooke, Beih. Sydowia 4: 43. 1961.

≡ *Lachnella totara* (G. Cunn.) G. Cunn., New Zealand Dept.

Sci. Industr. Res., Bull. 145: 318. 1963.

TYPE HOST: *Podocarpus totara* D. Don (*Podocarpaceae*).

ETYMOLOGY: **tōtara**, Māori name (and common name) for *Podocarpus totara* and *P. laetus*.

Peniophora totara G. Cunn., Trans. Roy. Soc. New Zealand 83: 271. 1955.

≡ *Phlebia totara* (G. Cunn.) Stalpers & P.K. Buchanan,
New Zealand J. Bot. 29: 338. 1991.

TYPE HOST: *Podocarpus hallii* (*Podocarpaceae*) [= *Podocarpus laetus* Hooibr. ex Endl.].

ETYMOLOGY: **tōtara**, Māori name (and common name) for *Podocarpus laetus* and *P. totara*.

Poria totara G. Cunn., New Zealand Dept. Sci. Industr. Res., Bull. 164: 261. 1965.

≡ *Ceriporia totara* (G. Cunn.) P.K. Buchanan & Ryvarden, Mycotaxon 31: 33. 1988.

≡ *Gloeoporus totara* [as “*totarus*”] (G. Cunn.) Zmitr. & Spirin, Mycena 6: 36. 2006.

TYPE HOST: *Podocarpus totara* D. Don (*Podocarpaceae*).

ETYMOLOGY: **tōtara**, Māori name (and common name) for *Podocarpus totara* and *P. laetus*.

tupare

Uredo tupare G. Cunn., Trans. & Proc. New Zealand Inst. 55: 44. 1924.

TYPE HOST: *Olearia colensoi* Hook.f. (*Oleaceae*).

ETYMOLOGY: **tūpare**, Māori name for *Olearia colensoi*.

waiouru

Cintractia waiouru G. Cunn., Trans. & Proc. Roy. Soc. New Zealand 75: 335. 1945.

TYPE HOST: *Carpha alpina* R. Br. (*Cyperaceae*).

ETYMOLOGY: **waiouru**, Māori; referring to the area south of the type locality, Waihohonu Stream, National Park, Taupo.

= *Anthracoidea carphae* (Speg.) Vánky, Bot. Not. 132: 230. 1979.

weraroensis

Poria weraroensis G. Cunn., New Zealand Dept. Sci. Industr. Res., Pl. Dis. Div.,
Bull. 72: 40. 1947, nom. dub.

[a name of uncertain application; Buchanan & Ryvarden 2000: 301].

ETYMOLOGY: **weraroa**, Māori; referring to the type locality, Weraroa, Wellington.

whakatipu

Puccinia whakatipu G. Cunn., Trans. & Proc. New Zealand Inst. 55: 4. 1924.

TYPE HOST: *Anisotome filifolia* (Hook.f.) Cockayne & Laing (*Umbelliferae*).

ETYMOLOGY: **whakatipu/wakatipu**, Māori; referring to the type locality, Lake Wakatipu, Otago Lakes.

wharanui

Uredo wharanui G. Cunn., Trans. & Proc. New Zealand Inst. 55: 46. 1924.

TYPE HOST: *Olearia insignis* (*Compositae*) [= *Pachystegia insignis* (Hook.f.) Cheeseman].

ETYMOLOGY: **wharanui**, Māori; referring to the type locality, Wharanui, Kaikoura.

TABLE 1. Fungal generic names based on te reo Māori.
Classification is to family and order; '[L]' = lichenised taxon.

NAME	TAXON	CLASSIFICATION
<i>Aotearoamycetes</i>	<i>Aotearoamycetes</i> P.R. Johnst. & al. 2018	<i>Tympanidaceae</i> , <i>Helotiales</i>
<i>Harorepupu</i>	<i>Harorepupu</i> P.R. Johnst. & al. 2015	Inc. sed., <i>Onygenales</i>
<i>Podotara</i>	<i>Podotara</i> Malcolm & Vězda 1996	<i>Pilocarpaceae</i> , <i>Lecanorales</i> [L]
<i>Pureke</i>	<i>Pureke</i> P.R. Johnst. 1991	<i>Rhytismataceae</i> , <i>Rhytismatales</i>
<i>Weraroa</i>	<i>Weraroa</i> Singer 1958	<i>Hymenogastraceae</i> , <i>Agaricales</i>

TABLE 2. Fungal species and variety epithets based on te reo Māori and ta re Moriori; only new and replacement names are listed.
Classification is to subphylum; [L] = lichenised taxon; [Lc] = lichenicolous taxon.

EPITHET	TAXON	CLASSIFICATION
<i>akatorensis</i>	<i>Buellia akatorensis</i> Elix & A. Knight 2017	<i>Pezizomycotina</i> [L]
<i>akiraho</i>	<i>Puccinia akiraho</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>anauensis</i>	<i>Cortinarius anauensis</i> Soop 2001	<i>Agaricomycotina</i>
<i>aorangi</i>	<i>Puccinia aorangi</i> G. Cunn. 1930	<i>Agaricomycotina</i>
	<i>Stephanospora aorangi</i> Beever & al. 2015	<i>Pucciniomycotina</i>
<i>aotearoa</i>	<i>Armillaria aotearoa</i> L.A. Hood & Ramsfield 2016	<i>Agaricomycotina</i>
	<i>Chalara aotearoa</i> Nag Raj & S. Hughes 1974	<i>Pezizomycotina</i>
	<i>Colletotrichum aotearoa</i> B.S. Weir & P.R. Johnst. 2012	<i>Pezizomycotina</i>
	<i>Harorepupu aotearoa</i> P.R. Johnst. & al. 2015	<i>Pezizomycotina</i>
	<i>Lachnella aotearoa</i> G. Cunn. 1963	<i>Agaricomycotina</i>
	<i>Neopestalotiopsis aotearoa</i> Maharachch. & al. 2014	<i>Pezizomycotina</i>
	<i>Phyllisciella aotearoa</i> Henssen & J.K. Bartlett 1984	<i>Pezizomycotina</i> [L]
	<i>Stereum aotearoa</i> G. Cunn. 1956	<i>Agaricomycotina</i>
<i>aotearoae</i>	<i>Chaetosphaeria aotearoae</i> S. Hughes 1966	<i>Pezizomycotina</i>
	<i>Hypochnicium aotearoae</i> B.C. Paulus & al. 2007	<i>Agaricomycotina</i>
	<i>Neotyphodium aotearoae</i> C.D. Moon & al. 2002	<i>Pezizomycotina</i>
	<i>Penicillium aotearoae</i> Visagia & Seifert 2016	<i>Pezizomycotina</i>
<i>aotearoana</i>	<i>Pannaria aotearoana</i> Elvebakk & Elix 2016	<i>Pezizomycotina</i> [L]
<i>araniiti</i>	<i>Cortinarius araniiti</i> Soop 2014	<i>Agaricomycotina</i>
<i>aroa</i>	<i>Poria aroa</i> G. Cunn. 1947	<i>Agaricomycotina</i>
<i>awakinoana</i>	<i>Chlorociboria awakinoana</i> P.R. Johnst. 2005	<i>Pezizomycotina</i>
<i>awhitu</i>	<i>Fomes awhitu</i> G. Cunn. 1948	<i>Agaricomycotina</i>
<i>corokiae</i>	<i>Septoria corokiae</i> Henn.1898	<i>Pezizomycotina</i>
<i>hakaroa</i>	<i>Gymnopus hakaroa</i> J.A. Cooper & P. Leonard 2013	<i>Agaricomycotina</i>
<i>harakeke</i>	<i>Marthamyces harakeke</i> P.R. Johnst. 2019	<i>Pezizomycotina</i>
<i>haumata</i>	<i>Uredo haumata</i> G. Cunn. 1928	<i>Pucciniomycotina</i>
<i>hautu</i>	<i>Hysterangium hautu</i> G. Cunn. 1938	<i>Agaricomycotina</i>
<i>hautuensis</i>	<i>Protuberia hautuensis</i> Castellano & Beever 1994	<i>Agaricomycotina</i>
<i>hauturu</i>	<i>Cordyceps hauturu</i> Dingley 1953	<i>Pezizomycotina</i>
	<i>Nectria hauturu</i> Dingley 1951	<i>Pezizomycotina</i>
	<i>Phyllachora hauturu</i> P.R. Johnst. & P.F. Cannon 2004	<i>Pezizomycotina</i>
<i>hauturuanum</i>	<i>Lophodermium hauturuanum</i> P.R. Johnst. 1989	<i>Pezizomycotina</i>

EPITHET	TAXON	CLASSIFICATION
<i>heketara</i>	<i>Puccinia heketara</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>hoheriae</i>	<i>Eichleriella hoheriae</i> McNabb 1969	<i>Agaricomycotina</i>
	<i>Irenopsis hoheriae</i> Hansf. 1955	<i>Pezizomycotina</i>
	<i>Myxosporium hoheriae</i> J.D. Atk. 1940	<i>Pezizomycotina</i>
	<i>Nectria hoheriae</i> Dingley 1989	<i>Pezizomycotina</i>
	<i>Puccinia hoheriae</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
	<i>Puccinia hoheriae</i> Wakef. 1917	<i>Pucciniomycotina</i>
<i>horoeka</i>	<i>Pirottaea horoeka</i> P.R. Johnst. 1998	<i>Pezizomycotina</i>
<i>horopito</i>	<i>Uredo horopito</i> G. Cunn. 1945	<i>Pucciniomycotina</i>
<i>huia</i>	<i>Solenia huia</i> G. Cunn. 1953	<i>Agaricomycotina</i>
<i>huiaensis</i>	<i>Bullera huiaensis</i> Hamam. & Nakase 1996	<i>Agaricomycotina</i>
<i>hunua</i>	<i>Hypocrea hunua</i> Dingley 1952	<i>Pezizomycotina</i>
	<i>Poria hunua</i> G. Cunn. 1947	<i>Agaricomycotina</i>
<i>hupiro</i>	<i>Aecidium hupiro</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>iringa</i>	<i>Cortinarius iringa</i> Soop 2003	<i>Agaricomycotina</i>
<i>iti</i>	<i>Rhodocybe iti</i> E. Horak 1979	<i>Agaricomycotina</i>
<i>itiiti</i>	<i>Microsporidium itiiti</i> L.A. Malone 1985	<i>Microsporidia</i>
<i>kaikawakae</i>	<i>Lophodermium kaikawakae</i> P.R. Johnst. 1989	<i>Pezizomycotina</i>
<i>kaiku</i>	<i>Caecoma kaiku</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>kaimanawa</i>	<i>Cortinarius kaimanawa</i> Soop 2003	<i>Agaricomycotina</i>
<i>kaitokensis</i>	<i>Strigolaitia kaitokensis</i> Sérus. & Polly 1996	<i>Pezizomycotina</i> [L]
<i>kamahi</i>	<i>Fuscoporia kamahi</i> G. Cunn. 1965	<i>Agaricomycotina</i>
<i>kamaka</i>	<i>Clitopilus kamaka</i> J.A. Cooper 2014	<i>Agaricomycotina</i>
<i>kanuka</i>	<i>Hydnangium kanuka</i> J.A. Cooper 2014	<i>Agaricomycotina</i>
	<i>Stephanospora kanuka</i> T. Lebel & Castellano 2015	<i>Agaricomycotina</i>
<i>kanukaneus</i>	<i>Marasmius kanukaneus</i> G. Stev. 1964	<i>Agaricomycotina</i>
<i>kapiti</i>	<i>Anthostomella kapiti</i> Whitton & al. 2000	<i>Pezizomycotina</i>
	<i>Stachybotrys kapiti</i> Whitton & al. 2001	<i>Pezizomycotina</i>
<i>kapitiae</i>	<i>Anthostomella kapitiae</i> Whitton & al. 2000	<i>Pezizomycotina</i>
<i>kapitiana</i>	<i>Niesslia kapitiana</i> Whitton & al. 2012	<i>Pezizomycotina</i>
<i>karaka</i>	<i>Cercospora karaka</i> G.F. Laundon 1973	<i>Pezizomycotina</i>
<i>karea</i>	<i>Amanita karea</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>karetu</i>	<i>Uredo karetu</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>kauri</i>	<i>Corticium kauri</i> G. Cunn. 1954	<i>Agaricomycotina</i>
<i>keae</i>	<i>Puccinia keae</i> G. Cunn. 1928	<i>Pucciniomycotina</i>
<i>kiko</i>	<i>Hymenoscyphus kiko</i> P.R. Johnst. 2013	<i>Pezizomycotina</i>
<i>kiwiorum</i>	<i>Austrostromium kiwiorum</i> M.C. Williams & Lichtw. 1990	<i>Kickxellomycotina</i>
<i>koherika</i>	<i>Puccinia koherika</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>kohu</i>	<i>Lecanora kohu</i> Printzen & al. 2017	<i>Pezizomycotina</i> [L]
<i>konini</i>	<i>Uredo konini</i> G. Cunn. 1928	<i>Pucciniomycotina</i>
<i>kopoti</i>	<i>Puccinia kopoti</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
<i>kopuwaianus</i>	<i>Tetramelas kopuwaianus</i> Elix & H. Mayrhofer 2018	<i>Pezizomycotina</i> [L]

EPITHET	TAXON	CLASSIFICATION
<i>kowhai</i>	<i>Aecidium kowhai</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
	<i>Clonostachys kowhai</i> Schroers 2001	<i>Pezizomycotina</i>
	<i>Nectria kowhai</i> Dingley 1956	<i>Pezizomycotina</i>
<i>kukutae</i>	<i>Phaeosphaeria kukutae</i> G.S. Ridl. 1988	<i>Pezizomycotina</i>
<i>mahinapua</i>	<i>Pirottaea mahinapua</i> P.R. Johnst. 1998	<i>Pezizomycotina</i>
<i>mahinapuense</i>	<i>Sarcostroma mahinapuense</i> Gadgil & M.A. Dick 1999	<i>Pezizomycotina</i>
<i>mahuianum</i>	<i>Lophodermium mahuianum</i> P.R. Johnst. 1989	<i>Pezizomycotina</i>
<i>maire</i>	<i>Laricifomes maire</i> G. Cunn. 1965	<i>Agaricomycotina</i>
<i>makarorae</i>	<i>Psilocybe makarorae</i> P.R. Johnst. & P.K. Buchanan 1995	<i>Agaricomycotina</i>
<i>mamaku</i>	<i>Mycena mamaku</i> Segedin 1991	<i>Agaricomycotina</i>
<i>manawaorae</i>	<i>Ascochyta manawaorae</i> Verkley & al. 2010	<i>Pezizomycotina</i>
<i>manawatua</i>	<i>Anthostomella manawatua</i> Whitton & al. 2000	<i>Pezizomycotina</i>
<i>mangatepopense</i>	<i>Lophodermium mangatepopense</i> P.R. Johnst. 1989	<i>Pezizomycotina</i>
<i>mania</i>	<i>Puccinia mania</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>manuka</i>	<i>Hypocrea manuka</i> Dingley 1952	<i>Pezizomycotina</i>
	<i>Nectria manuka</i> Dingley 1951	<i>Pezizomycotina</i>
	<i>Phyllachora manuka</i> P.R. Johnst. & P.F. Cannon 2004	<i>Pezizomycotina</i>
	<i>Poria manuka</i> G. Cunn. 1947	<i>Agaricomycotina</i>
<i>manukanea</i>	<i>Astrosporina manukanea</i> E. Horak 1978	<i>Agaricomycotina</i>
<i>marama</i>	<i>Debaryomyces marama</i> di Menna 1954	<i>Saccharomycotina</i>
<i>maruiaensis</i>	<i>Lactarius maruiaensis</i> McNabb 1971	<i>Agaricomycotina</i>
<i>maungahukae</i>	<i>Lecideia lapicida</i> var. <i>maungahukae</i> Hertel 2001	<i>Pezizomycotina</i> [L]
<i>maungatautari</i>	<i>Ellisembia maungatautari</i> McKenzie 2010	<i>Pezizomycotina</i>
	<i>Solicorynespora maungatautari</i> McKenzie 2010	<i>Pezizomycotina</i>
<i>maungatuensis</i>	<i>Buellia maungatuensis</i> Elix & H. Mayrhofer 2017	<i>Pezizomycotina</i> [L]
<i>maurea</i>	<i>Puccinia maurea</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>mumura</i>	<i>Amanita mumura</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>murihikuana</i>	<i>Umbilicaria murihikuana</i> D.J. Galloway & L.G. Sancho 2005	<i>Pezizomycotina</i> [L]
<i>muritai</i>	<i>Lepista muritai</i> G. Stev. 1964	<i>Agaricomycotina</i>
<i>muritaiensis</i>	<i>Hygrophorus muritaiensis</i> G. Stev. 1963	<i>Agaricomycotina</i>
<i>namua</i>	<i>Puccinia namua</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>nehuta</i>	<i>Amanita nehuta</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>ngohengohe</i>	<i>Rhodotorula ngohengohe</i> Padamsee & al. 2017	<i>Pucciniomycotina</i>
<i>nikau</i>	<i>Epithele nikau</i> G. Cunn. 1956	<i>Agaricomycotina</i>
	<i>Lachnella nikau</i> G. Cunn. 1963	<i>Agaricomycotina</i>
	<i>Peniophora nikau</i> G. Cunn. 1963	<i>Agaricomycotina</i>
	<i>Sebacina nikau</i> McNabb 1969	<i>Agaricomycotina</i>
<i>ohakune</i>	<i>Hymenoscyphus ohakune</i> P.R. Johnst. 2013	<i>Pezizomycotina</i>
<i>ohauensis</i>	<i>Thaxterogaster ohauensis</i> Soop 1998	<i>Agaricomycotina</i>
<i>okatina</i>	<i>Anthostomella okatina</i> Whitton & al. 2000	<i>Pezizomycotina</i>
<i>omahutaense</i>	<i>Sporidesmium omahutaense</i> Matsush. 1985	<i>Pezizomycotina</i>
<i>oratiensis</i>	<i>Mycena oratiensis</i> Segedin 1991	<i>Agaricomycotina</i>

EPITHET	TAXON	CLASSIFICATION
<i>orokonuiiana</i>	<i>Megalaria orokonuiiana</i> Fryday & A. Knight 2012	<i>Pezizomycotina</i> [L]
<i>otagensis/-ense</i>	<i>Acarospora otagensis</i> H. Magn. 1943	<i>Pezizomycotina</i> [L]
	<i>Aecidium otagensis</i> Linds. 1867	<i>Pucciniomycotina</i>
	<i>Buellia otagensis</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
	<i>Corticium otagensis</i> G. Cunn. 1963	<i>Agaricomycotina</i>
	<i>Lecidea otagensis</i> Nyl. 1867	<i>Pezizomycotina</i> [L]
	<i>Marasmius otagensis</i> G. Stev. 1964	<i>Agaricomycotina</i>
	<i>Melanospora otagensis</i> Linds. 1867	<i>Pezizomycotina</i> [L]
	<i>Nectria otagensis</i> Linds. 1867	<i>Pezizomycotina</i>
	<i>Parmelia otagensis</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
	<i>Pellicularia otagensis</i> G. Cunn. 1953	<i>Agaricomycotina</i>
	<i>Porina otagensis</i> P.M. McCarthy 1999	<i>Pezizomycotina</i> [L]
	<i>Sphaeria otagensis</i> Linds. 1867	<i>Pezizomycotina</i>
	<i>Verrucaria otagensis</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
<i>otagoana</i>	<i>Lecidea otagoana</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
	<i>Pertusaria otagoana</i> D.J. Galloway 1983	<i>Pezizomycotina</i> [L]
<i>otagoensis/-ense</i>	<i>Coniocybe otagoensis</i> Js. Murray 1960	<i>Pezizomycotina</i>
	<i>Leucopaxillus otagoensis</i> G. Stev. 1964	<i>Agaricomycotina</i>
	<i>Ramalina otagoensis</i> W. Martin & J. Child 1972	<i>Pezizomycotina</i> [L]
<i>otakou</i>	<i>Poria otakou</i> G. Cunn. 1947	<i>Agaricomycotina</i>
	<i>Uromyces otakou</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
<i>otira</i>	<i>Aecidium otira</i> G. Cunn. 1928	<i>Pucciniomycotina</i>
<i>pahiensis</i>	<i>Lecidea pahiensis</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
<i>papakaiensis</i>	<i>Russula papakaiensis</i> McNabb 1973	<i>Agaricomycotina</i>
<i>papakurae</i>	<i>Circinotrichum papakurae</i> S. Hughes & Piroz. 1971	<i>Pezizomycotina</i>
<i>papanui</i>	<i>Buellia papanui</i> Elix & H. Mayrhofer 2017	<i>Pezizomycotina</i> [L]
	<i>Caloplaca papanui</i> D.J. Galloway 2004	<i>Pezizomycotina</i> [L]
<i>paraoniti</i>	<i>Cortinarius paraoniti</i> Soop 2013	<i>Agaricomycotina</i>
<i>paraonui</i>	<i>Cortinarius paraonui</i> Soop 2005	<i>Agaricomycotina</i>
<i>pareparina</i>	<i>Amanita pareparina</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>patearoana</i>	<i>Buellia patearoana</i> Elix & A. Knight 2017	<i>Pezizomycotina</i> [L]
<i>pekeoides</i>	<i>Amanita pekeoides</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>pirongia</i>	<i>Poria pirongia</i> G. Cunn. 1947	<i>Agaricomycotina</i>
<i>poropingao</i>	<i>Stephanospora poropingao</i> T. Lebel & Castellano	<i>Agaricomycotina</i>
<i>pounamu</i>	<i>Hispidula pounamu</i> P.R. Johnst. 2003	<i>Pezizomycotina</i>
	<i>Puccinia pounamu</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
	<i>Stephanospora pounamu</i> T. Lebel & Castellano 2015	<i>Agaricomycotina</i>
<i>poutoensis</i>	<i>Chlorociboria poutoensis</i> P.R. Johnst. 2005	<i>Pezizomycotina</i>
<i>puawhananga</i>	<i>Uredo puawhananga</i> G.T.S. Baylis 1954	<i>Pucciniomycotina</i>
<i>pumatona</i>	<i>Amanita pumatona</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>rakiurae</i>	<i>Parmeliella rakiurae</i> P.M. Jørg. & D.J. Galloway 2004	<i>Pezizomycotina</i> [L]
<i>rangitatensis</i>	<i>Amandinea rangitatensis</i> Elix & H. Mayrhofer 2017	<i>Pezizomycotina</i> [L]
<i>rapua</i>	<i>Microsporidium rapua</i> J.B. Jones 1981	<i>Microsporidia</i>
<i>rata</i>	<i>Poria rata</i> G. Cunn. 1947	<i>Agaricomycotina</i>

EPITHET	TAXON	CLASSIFICATION
<i>rautahi</i>	<i>Puccinia rautahi</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>rekohu</i>	<i>Phyllachora hauturu</i> subsp. <i>rekohu</i> P.R. Johnst. & P.F. Cannon 2004	<i>Pezizomycotina</i>
<i>rimuphilus</i>	<i>Marasmius rimuphilus</i> Desjardin & E. Horak 1997	<i>Agaricomycotina</i>
<i>rimutaka</i>	<i>Collybia rimutaka</i> G. Stev. 1964	<i>Agaricomycotina</i>
<i>rongomai-pounamu</i>	<i>Candida rongomai-pounamu</i> Padamsee & al. 2017	<i>Saccharomycotina</i>
<i>rotoruaensis</i>	<i>Chytrium rutoruaensis</i> Karling 1970	<i>Chytridiomycotina</i>
<i>ruapehu</i>	<i>Nectria ruapehu</i> Dingley 1951	<i>Pezizomycotina</i>
<i>taiepa</i>	<i>Amanita taiepa</i> G.S. Ridl. 1991	<i>Agaricomycotina</i>
<i>takapauensis</i>	<i>Nosema takapauensis</i> I.M. Hall & al. 1976	<i>Microsporidia</i>
<i>takoropuku</i>	<i>Elsinoe takoropuku</i> G.S. Ridl. & Ramsfield 2006	<i>Pezizomycotina</i>
<i>tapawera</i>	<i>Macowanites tapawera</i> T. Lebel 2002	<i>Agaricomycotina</i>
<i>tararua</i>	<i>Puccinia tararua</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
<i>tararuana</i>	<i>Lecanora tararuana</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
<i>tararuensis</i>	<i>Lecidea tararuensis</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
<i>taupoensis</i>	<i>Sporobolomyces taupoensis</i> Hamam. & Nakase 1995	<i>Pucciniomycotina</i>
<i>tawa</i>	<i>Hypocrea tawa</i> Dingley 1952	<i>Pezizomycotina</i>
	<i>Nectria tawa</i> Dingley 1951	<i>Pezizomycotina</i>
	<i>Sebacina tawa</i> McNabb 1969	<i>Agaricomycotina</i>
	<i>Trametes tawa</i> G. Cunn. 1948	<i>Agaricomycotina</i>
	<i>Tremella tawa</i> McNabb 1990	<i>Agaricomycotina</i>
	<i>Trichoderma tawa</i> P. Chaverri & Samuels 2003	<i>Pezizomycotina</i>
<i>tawai</i>	<i>Lactarius tawai</i> McNabb 1971	<i>Agaricomycotina</i>
	<i>Russula tawai</i> McNabb 1973	<i>Agaricomycotina</i>
<i>tawhai</i>	<i>Fuscoporia tawhai</i> G. Cunn. 1948	<i>Agaricomycotina</i>
<i>tekapo</i>	<i>Puccinia tekapo</i> McNabb 1962	<i>Pucciniomycotina</i>
<i>ti</i>	<i>Colletotrichum ti</i> B.S. Weir & P.R. Johnst. 2012	<i>Pezizomycotina</i>
<i>tiritea</i>	<i>Puccinia tiritea</i> G. Cunn. 1923	<i>Pucciniomycotina</i>
<i>toa</i>	<i>Puccinia toa</i> G. Cunn. 1930	<i>Pucciniomycotina</i>
<i>toatoa</i>	<i>Tyromyces toatoa</i> G. Cunn. 1965	<i>Agaricomycotina</i>
<i>toetoe</i>	<i>Uredo toetoe</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>tokerau</i>	<i>Hispidula tokerau</i> P.R. Johnst. 2003	<i>Pezizomycotina</i>
<i>tongariro</i>	<i>Cyphella tongariro</i> G. Cunn. 1953	<i>Agaricomycotina</i>
<i>toro</i>	<i>Hypocrea toro</i> Dingley 1952	<i>Pezizomycotina</i>
<i>totara</i>	<i>Cyphella totara</i> G. Cunn. 1953	<i>Agaricomycotina</i>
	<i>Peniophora totara</i> G. Cunn. 1955	<i>Agaricomycotina</i>
	<i>Poria totara</i> G. Cunn. 1965	<i>Agaricomycotina</i>
<i>tatarae</i>	<i>Auricula tatarae</i> Lloyd 1920	<i>Agaricomycotina</i>
	<i>Hysterium pulicare</i> subsp. <i>tatarae</i> Sacc. 1908	<i>Pezizomycotina</i>
	<i>Lecanactis tatarae</i> Zahlbr. 1941	<i>Pezizomycotina</i> [L]
<i>totaranuiensis</i>	<i>Scutellinia totaranuiensis</i> J. Moravec 1996	<i>Pezizomycotina</i>
<i>tuapekensis</i>	<i>Buellia tuapekensis</i> Elix & A. Knight 2017	<i>Pezizomycotina</i> [L]

EPITHET	TAXON	CLASSIFICATION
<i>tuku</i>	<i>Ramomarthamyces tuku</i> P.R. Johnst.	<i>Pezizomycotina</i>
<i>tupare</i>	<i>Uredo tupare</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>umerensis</i>	<i>Lactarius umerensis</i> McNabb 1971	<i>Agaricomycotina</i>
	<i>Russula umerensis</i> McNabb 1973	<i>Agaricomycotina</i>
<i>ura</i>	<i>Mycena ura</i> Segedin 1991	<i>Agaricomycotina</i>
<i>urewera</i>	<i>Zanclospora urewera</i> J.A. Cooper 2005	<i>Pezizomycotina</i>
<i>waikaia</i>	<i>Hymenoscyphus waikaia</i> P.R. Johnst. 2013	<i>Pezizomycotina</i>
<i>waikanaensis</i>	<i>Hygrophorus waikanaensis</i> G. Stev. 1963	<i>Agaricomycotina</i>
	<i>Phaeosphaeria waikanaensis</i> G.S. Ridl. 1988	<i>Pezizomycotina</i>
<i>waikaremoana</i>	<i>Entoloma waikaremoana</i> E. Horak 2008	<i>Agaricomycotina</i>
<i>waiouru</i>	<i>Cintractia waiouru</i> G. Cunn. 1945	<i>Ustilaginomycotina</i>
<i>waiporianus</i>	<i>Cortinariu waiporianu</i> Soop 2013	<i>Agaricomycotina</i>
<i>waiporiensis</i>	<i>Leucopaxillus waiporiensis</i> G. Stev. 1964	<i>Agaricomycotina</i>
	<i>Parmelia waiporiensis</i> Hillmann 1938	<i>Pezizomycotina</i> [L]
<i>waipoua</i>	<i>Uromyces waipoua</i> McNabb 1966	<i>Pucciniomycotina</i>
<i>waitakere</i>	<i>Stachybotrys waitakere</i> Whitton & al. 2001	<i>Pezizomycotina</i>
<i>waitemataensis</i>	<i>Niesslia waitemataensis</i> W. Gams & al. 2019	<i>Pezizomycotina</i>
<i>wakatipu</i>	<i>Anthracoidea wakatipu</i> Vánky 2000	<i>Ustilaginomycotina</i>
<i>weraroa</i>	<i>Psilocybe weraroa</i> Borov. & al.	<i>Agaricomycotina</i>
<i>weraroensis</i>	<i>Poria weraroensis</i> G. Cunn. 1947	<i>Agaricomycotina</i>
<i>whakapapaensis</i>	<i>Sphaerophorus whakapapaensis</i> Wedin 1991	<i>Pezizomycotina</i> [L]
<i>whakatipae</i>	<i>Lecidea whakatipae</i> C. Knight 1876	<i>Pezizomycotina</i> [Lc]
<i>whakatipu</i>	<i>Puccinia whakatipu</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>wharanui</i>	<i>Uredo wharanui</i> G. Cunn. 1924	<i>Pucciniomycotina</i>
<i>wheroparaonea</i>	<i>Limacella wheroparaonea</i> G.S. Ridl. 1993	<i>Agaricomycotina</i>

Discussion

Pre-Cunningham use of te reo Māori

The earliest te reo-derived fungal epithet was *otagensis/otagense*, used for five specimens (two lichens, two unlichenised ascomycetes, and a spectacular rust affecting puāwhānanga [*Clematis paniculata*] blossoms) collected by Scottish lichenologist William Lauder Lindsay during an extended visit to Otago Province, and later described by Lindsay (1867) and Nylander (1867). A lichenicolous fungus was described by New Zealand-resident lichenologist Charles Knight (1876) as *Lecidea whakatipae*; the epithet refers to Wakatipu, one of the Otago Lakes, probably the vicinity of the unlisted type locality. The only other 19th century te reo-derived epithet was a pathogen of a korokio tree [*Corokia buddleioides*] growing in Germany and described by German mycologist Paul Hennings (1899) as *Septoria "corockeae"* (correctly *corokiae*;

Turland & al. 2018: Art. F.9.1). In the early 20th century, three more te reo-derived epithets were published: *Hysterium pulicare* subsp. *totarae* on a tōtara tree [*Podocarpus totara*] growing in Italy (Saccardo 1908); *Puccinia hoheriae* on a specimen of hōhere [*Hoheria populnea*] sent to Kew, England for fungal identification (Wakefield 1917); and *Auricula totarae* on dead tōtara wood sent to USA for fungal identification (Lloyd 1920).

Use of te reo Māori by Cunningham and his successors

Cunningham began proposing te reo Māori epithets in his first paper on rust fungi in New Zealand (Cunningham 1923) and continued to do so until his two posthumously published monographs (Cunningham 1963, 1965). His example has inspired numerous subsequent New Zealand mycologists (and others working on New Zealand fungi) to use te reo Māori and ta re Moriori [the indigenous language of Rēkohu/Chatham Islands, New Zealand] as the basis of new fungal names. A total of 231 such fungal names: five genera (TABLE 1); and 226 species/subspecies/varieties (TABLE 2), have been located, and are listed either as published or with minor orthographic corrections required to comply with the International Code of Nomenclature for algae, fungi, and plants (ICN; Turland & al. 2020). Although Veale & al. (2019: Appendix S1) published a “List of taxa recorded with te reo / ta re epithets”, this included only one fungal genus and 140 fungal species/subspecies (i.e., 90 names, including 14 of Cunningham’s 56 species, were omitted); their list contained several misspellings and miscitations, as well as three entries that have no connection with te reo Māori (*ackamae* refers to the host genus *Ackama*, which is an anagram; *horakii* honours Austrian mycologist Egon Horak, who has been collecting and describing New Zealand agarics for more than 50 years; and *Waitea* refers to the Waite Research Institute, Adelaide, Australia).

Nomenclatural use of te reo Māori and other non-latin languages

The majority of the published te reo Māori epithets have been treated as undeclinable adjectives or nouns in apposition, preserving the authentic te reo Māori orthography (apart from the problem of “long” vowels indicated by macron diacritical marks; see next section, below). The presentation of vernacular epithets as nouns in apposition has a tradition dating from the birth of botanical nomenclature: Linnaeus (1753) published numerous examples, e.g., *Calamus rotang* L., rattan; *Piper betle* L., betel nut; *Theobroma cacao* L., cacao [cocoa]. Other te reo Māori epithets have been modified in what appear to be misguided attempts to convert

them into “Latin” adjectives or genitive nouns. Like the majority of non-European vernacular languages, te reo Māori does not conform to the latinate word-model of a linguistic stem + a declinable inflection that indicates grammatical case, gender, number, etc. Attempts to modify vernacular words according to latinate grammatical conventions result in the creation of chimaeras that convey no Latin meaning and mangle the vernacular word. Every syllable in te reo Māori words consists of a vowel (with or without a preceding consonant); removal of the final vowel from a word does not create a “linguistic stem”, but rather it deletes either the whole of the final syllable or leaves a final consonant deprived of its vowel, distorting the pronunciation and meaning of the word and diminishing its mana [status; prestige; spirituality].

Nomenclatural use of te reo Māori macron-vowels

In modern orthography, te reo Māori vowels are differentiated as short [“a/e/i/o/u”] or long [either “aa/ee/ii/oo/uu”, or “ā/ē/ī/ō/ū”]. ICN Art. 60.7 (Turland & al. 2020) requires the suppression of all diacritical letters; therefore the macron-vowel orthography is not permitted, but the double-vowel orthography would be acceptable as “necessary transcriptions” of the macron-vowels. Veale & al. (2019) reached the same conclusion, in spite of having misinterpreted and mistranscribed Art. 60.7. It is diacritical signs (including macrons) that are forbidden, because the diacritical letters are additions to the basic Latin alphabet; the diaeresis, two dots placed over the second of two adjacent vowels, is permitted as an **optional** phonetic device to indicate the separate pronunciation of the two vowels. (Confusion often arises because the typographies of the diacritical umlaut and the non-diacritical diaeresis are identical.)

Place name epithets in te reo Māori and other non-latin languages

There is no reason why epithets derived from vernacular place names cannot also be presented as nouns in apposition; as discussed above, they should not be presented as “Latin” genitive nouns. However, place names in all languages are routinely formed into adjectival epithets by adding one of the geographical Latin suffixes recommended by ICN Rec. 60D.1 (Turland & al. 2020). For vernacular place names, this is an acceptable alternative to the preferred noun in apposition epithets, provided the place names are not abridged to create spurious “linguistic stems”; for te reo Māori place names, this means that the final vowel should always be retained before the geographical suffix is added, e.g., *awakinoana* from Awakino; *huiaensis* from Huia; and *weraroaensis* from Weraroa.

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Re-collection of secotioid *Entoloma calongei* in Europe

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ABSTRACT—In 2017, the secotioid *Entoloma calongei* was recorded in Slovakia, the first report since its Spanish holotype collection. Morphological and ecological characteristics are presented and compared with the type collection. LSU, mSSU, and ITS sequences were obtained and a combined maximum likelihood tree of SSU and LSU sequences was constructed.

KEY WORDS—*Entolomataceae*, taxonomy, *Rhodogaster*, sequestrate fungi, genetic distance

Introduction

In *Entoloma* sporocarp morphology is highly variable: ranging in size from tiny to large and in form as pleurotoid, omphalinoid, collybioid, mycenoid, tricholomatoid, and sequestrate. In the past, three smaller non-agaricoid genera have been distinguished based on habit: *Rhodocybella* T.J. Baroni & R.H. Petersen (cyphelloid), *Rhodogaster* E. Horak (secotioid), and *Richoniella* Costantin & L.M. Dufour (gasteroid).

The first record of a secotioid entolomatoid species was published by Horak (1963) from Chile, introducing a new monotypic genus for the species *Rhodogaster chilensis* E. Horak. In 1995, a similar collection found in Spain was initially misidentified as *R. chilensis* (Calonge & Pasabán 1995) but later recognized as a new species, *Rhodogaster calongei* (Horak & Moreno 1998).

Molecular phylogenetic studies of Co-David & al. (2009) placed the sequestrate genera *Richoniella* and *Rhodogaster* within *Entoloma*; and they transferred the two *Rhodogaster* species to *Entoloma*.

Entoloma calongei was recorded during field research in Lubovnianska Upland in NE Slovakia in 2017, and its identification has been confirmed by DNA sequence analyses. The Slovak collection represents only the second published record of this species.

Material & methods

SPECIMENS: Morphological and anatomical studies were conducted on fresh and dried basidiomata. Colours were determined according to Kornerup & Wanscher (1974). Microscopic features were studied in water or 3% KOH. All light micrographs of microscopic structures were made with a Nikon Eclipse Ni light microscope using bright field or differential interference contrast without staining, and images were captured with a Nikon DS-Ri2 digital camera. Images were processed and descriptive statistical analysis of basidiospore dimensions was produced using NIS-Elements BR 4.40 software. The voucher specimen was deposited in the herbarium of the Slovak National Museum-Natural History Museum, Bratislava, Slovakia (BRA).

DNA EXTRACTION, AMPLIFICATION AND SEQUENCING: DNA from the Slovakian *E. calongei* sporocarp was obtained from fresh material preserved in acetyl trimethylammonium bromide (CTAB) buffer and ground by using a plastic pestle and isolated by JENA Bioscience Blood-Animal-Plant DNA Preparation Kit following manufacture protocol. Target regions of the partial mitochondrial small subunit (mtSSU) rDNA and the nuclear large ribosomal subunit (LSU) were amplified using primers MS1/MS2 (White & al. 1990) and NL1/NL4 (Vilgalys & Hester 1990). The reaction was performed in 25 µl of reaction mixture containing 10 pmol of both primers, Crystal Hot Start Master, and 20 ng of template DNA. The cycling programme for mtSSU consisted of an initial denaturation at 94°C for 3 min, followed by 40 cycles of 94°C 30 s, 55°C for 30 s, 72°C for 1 min, and a final extension at 72°C for 5 min and for LSU of an initial denaturation at 95°C for 3 min, followed by 32 cycles of 95°C 30 s, 55°C for 30 s, 72°C for 1 min + increasing time 2 sec per cycle, and a final extension at 72°C for 10 min. The PCR products were purified using Qiagen columns (QIAquick PCR Purification Kit, Qiagen) according to the manufacturer's recommendations and sequenced commercially by Eurofins Genomics GmbH (Cologne, Germany).

ALIGNMENT AND PHYLOGENETIC ANALYSIS: DNA sequences of *Entolomataceae* and a selected *Clitocybe* outgroup were downloaded from NCBI on 18 January 2019. These included LSU and mtSSU sequences associated with Baroni & Matheny (2011). In total 15 LSU, and 15 mtSSU sequences were retrieved, including *E. calongei* type (TABLE 1). To these, we added newly generated LSU and mtSSU sequences from *Entoloma calongei* (BRACR30482). The tree was reconstructed by the maximum-

TABLE 1. *Entoloma* and *Clitocybe* sequences used for phylogenetic analysis (newly obtained sequences in **bold**).

SPECIES	COUNTRY	LSU	SSU	ITS
<i>C. dealbata</i>	Unknown	AF223175	DQ825431	—
<i>E. albidoquadratum</i> [holotype]	India	GQ289151	GQ289291	—
<i>E. calongei</i> [holotype]	Spain	GQ289158	GQ289298	—
<i>E. calongei</i> BRACR 30482	Slovakia	MK531556	MK530244	MK907407
<i>E. cocles</i>	Finland	GQ289159	GQ289299	—
<i>E. costatum</i>	Netherlands	GQ289161	GQ289301	—
<i>E. excentricum</i>	Germany	GQ289163	GQ289303	—
<i>E. gasteromycetoides</i>	New Zealand	GQ289164	GQ289304	—
<i>E. phaeomarginatum</i>	Tasmania	GQ289179	GQ289319	—
<i>E. porphyrescens</i>	Tasmania	GQ289182	GQ289322	—
<i>E. procerum</i>	Tasmania	GQ289183	GQ289323	—
<i>E. serricellum</i>	Belgium	GQ289190	GQ289330	—
<i>E. serrulatum</i>	Tasmania	GQ289192	GQ289332	—
<i>E. tectonicola</i> [holotype]	India	GQ289196	GQ289336	—
<i>E. transmutans</i>	Tasmania	GQ289200	GQ289340	—

likelihood method in MEGA-X with 1000 bootstrap replicates. The General Time Reversible model (Nei & Kumar 2000) with gamma-distributed evolutionary rates (G) and invariable sites (I) was chosen by MEGA as the best-fitting model. A matrix of inter-species distances was constructed using Kimura-2 parameter distances (Kimura 1980) in MEGA-X. We also produced an ITS barcode for *Entoloma calongei* (BRACR30482), now stored as SKDNA023-19 in BOLD v4 database (Barcode of Life Datasystems <http://v4.boldsystems.org/>).

Taxonomy

Entoloma calongei (E. Horak & G. Moreno) Noordel. & Co-David,

Persoonia 23: 166 (2009)

FIGS 1–3

≡ *Rhodogaster calongei* E. Horak & G. Moreno, Sydowia 50: 188 (1998)

PILEUS ≤25 mm diam., globose to subglobose (pyriform), margin involute and mostly attached to stipe, not expanding, greyish brown (8B1) with dark spots, silky and fibrillose, dry. STIPE short, with columella, ≤20 mm long, hollow, attenuated at base, silver grey (8B1), smooth, silky, fibrillose, dry. GLEBA irregularly labyrinthiform of reduced lamellae, non-gelatinized, lamellae greyish-white in section and pale pink (8B3) on surface. SMELL AND TASTE not distinctive. SPORE PRINT pink. BASIDIOSPORES cuboid or rhomboid (“pseudocuboid” sensu Karstedt & al. 2019), rarely pentagonal, (5.6–)6.3(–7.1) × (5.4–)6.8(–9.0) μm (Q = 0.80–1.01), often distorted, smooth, thin walled with distinct apiculus. Basidia 30 × 10 μm cylindrical to subclavate, 4 spored, clampless. Tramal hyphae short, cylindrical, clampless,



FIG. 1. *Entoloma calongei* (BRACR30482): a. In situ, 20.X.2017. (Photo: F. Fuljer); b. Sporocarps in cross section (Photo: A. Polhorský). Scale bar = 10 mm.

10–30 × 2–10 μm . PILEIPELLIS a cutis of cylindrical, narrow (80–100 × 5–6 μm), parallel clamppless hyphae, subcutis elements wider and shorter (40–80 × 15–20 μm).

SPECIMEN EXAMINED: SLOVAKIA, PREŠOV REGION, Lubovnianska Upland, Obručné village, 49.3080°N 20.9877°E, alt. 650 m, in grass in pasture, close to mixed forest, 20. X. 2017, leg. V. Kučera, det. V. Kautman (BRACR30482).

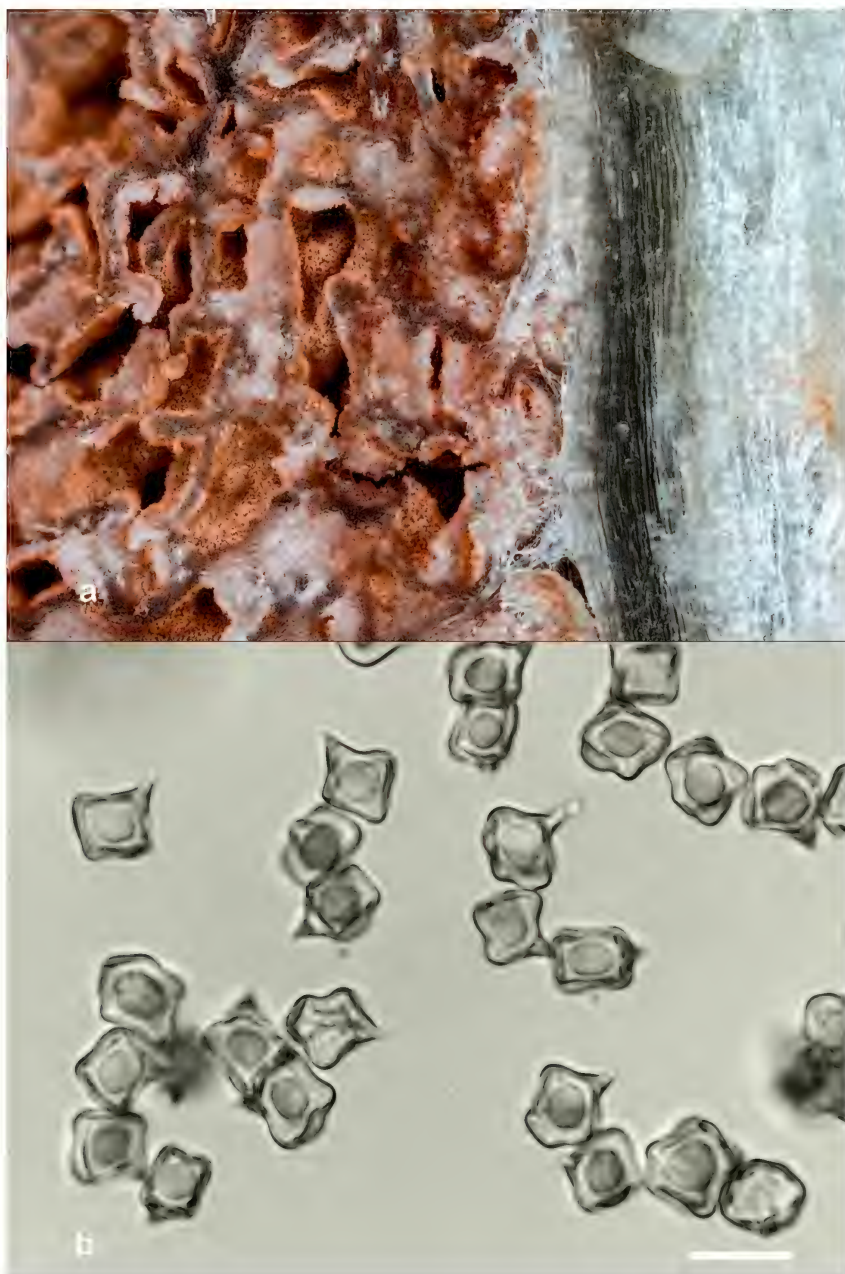


FIG. 2. *Entoloma calongei* (BRACR30482): a. Detail of gleba in cross section. (Photo: A. Polhorský); b. Spores (Photo: I. Kautmanová). Scale bar: a = 1 mm; b = 10 μ m.

HABITAT—Seminatural meadow mowed and/or grazed, southern slope; soil flysch sandy-silty, slightly basic but not calcareous. The specimens grew in grass, herbs (*Plantago*, *Trifolium*, *Taraxacum*), and mosses, ca 50 m from the edge of mixed forest (*Picea abies*, *Carpinus betulus*, *Fagus sylvatica*, *Corylus avellana*, *Cornus sanguinea*, *Betula*, *Acer*). The species was found in a rich grassland-fungi community together with various earth-tongues, waxcaps, and clavarioid fungi.

Discussion

Vidal & al. (2016) reported a total of 11 sequestrate *Entoloma* species, including four from Europe/Spain. Nine species were gasteroid and only two secotioid: *E. calongei* and *E. chilense* (E. Horak) Noordel. & Co-David. These two species differ from each other in a number of basic characters, including basidiospore morphology and pileipellis structure.

Basidiospores of *E. chilense* were described as “ellipsoidnodular” ($9.5\text{--}11.5 \times 7.5\text{ }\mu\text{m}$; Horak 1963), and those of *E. calongei* as cuboid (side lengths $6\text{--}10\text{ }\mu\text{m}$; Horak & Moreno 1998). Basidiospores of our collection were cuboid or rhomboid, often broader than long and side length is $6\text{--}8\text{ }\mu\text{m}$.

Although Horak (1963) described clamp connections as absent on basidia and tramal and cortical hyphae in the type description of *E. chilense*, Horak & Moreno (1998) later reported regularly observing clamp connections in *E. chilense*, contrasting with the clampless *E. calongei*. No clamp connections were observed in our specimens.

The pileipellis in the Slovak collections is a cutis composed of cylindrical parallel hyphae, the same as cited for *E. calongei* in the protologue and differing from the trichoderm of *E. chilense* (Horak 1963).

Ecology of the type localities of the two taxa was distinctly different. *Entoloma chilense* occurs among deep litter and humus in the coastal anectotrophic rain forest of Central Chile; the vegetation around the type locality was dominated by trees in *Lauraceae* and *Myrtaceae*, with *Chusquea* sp. (*Bambuseae*) in the understory (Horak 1963). By comparison, *E. calongei* was found in northern Spain in a colline-temperate mixed forest of conifers (*Larix*, *Pinus*) and broadleaf trees (*Fagus*, *Acer*, *Quercus*, *Fraxinus*, *Corylus*) at about 700 m a.s.l. (Calonge & Pasabán 1995). Our Slovakian collection site differed in that the basidiomata grew among grass and mosses in a pasture; however, the site was only 50 m from a forest composed of conifers and broadleaf trees similar to those in Spain.

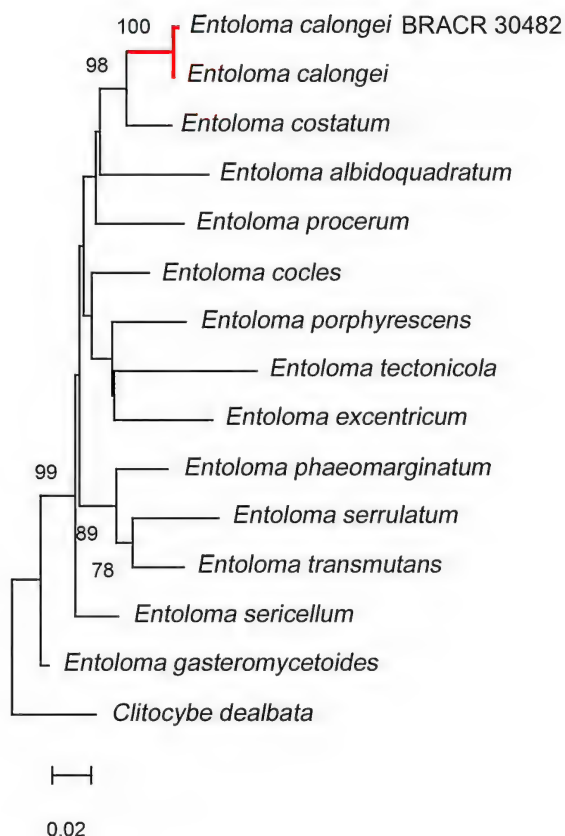


FIG. 3. Maximum likelihood phylogenetic tree constructed from the combined dataset (LSU+mtSSU). Red clade represents well-delimited species *Entoloma calongei*. *Clitocybe dealbata* was used as outgroup. Numbers above branches represent bootstrap support (only values >50% are shown).

It should be added that many *Entoloma* species occur both in semi-open forests and in grasslands without trees (Noordeloos 1992, 2004).

The sequence of *E. calongei* from Slovakia is almost identical with the type and the identity of Slovak collection has also been confirmed by using Kimura-2 parameter distances model. Our phylogeny (FIG. 3), like that of Co-David & al. 2009, places *E. calongei* close to *E. costatum* (Fr.) P. Kumm. with c. 3% dissimilarity (TABLE 2). *Entoloma costatum* is an extremely rare, rather fleshy, clitocybeoid species with rhomboid-

TABLE 2. Matrix of genetic inter-species distances from the *Entoloma* and *Clitocybe* sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1 <i>E. calongei</i> Slovakia	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
2 <i>E. calongei</i> Spain [Type]	0.001	—	—	—	—	—	—	—	—	—	—	—	—	—	—
3 <i>E. costatum</i>	0.043	0.035	—	—	—	—	—	—	—	—	—	—	—	—	—
4 <i>E. albidoquadratum</i>	0.062	0.060	0.059	—	—	—	—	—	—	—	—	—	—	—	—
5 <i>E. procerum</i>	0.065	0.055	0.052	0.065	—	—	—	—	—	—	—	—	—	—	—
6 <i>E. coctes</i>	0.054	0.047	0.052	0.066	0.051	—	—	—	—	—	—	—	—	—	—
7 <i>E. porphyrescens</i>	0.057	0.053	0.055	0.063	0.063	0.049	—	—	—	—	—	—	—	—	—
8 <i>E. tectonica</i>	0.079	0.078	0.082	0.092	0.076	0.075	0.064	—	—	—	—	—	—	—	—
9 <i>E. excentricum</i>	0.069	0.065	0.063	0.063	0.061	0.059	0.057	0.074	—	—	—	—	—	—	—
10 <i>E. phaeomarginatum</i>	0.066	0.055	0.054	0.060	0.050	0.049	0.056	0.076	0.065	—	—	—	—	—	—
11 <i>E. serrulatum</i>	0.081	0.070	0.075	0.080	0.067	0.063	0.067	0.083	0.072	0.051	—	—	—	—	—
12 <i>E. transmutans</i>	0.060	0.053	0.051	0.061	0.054	0.046	0.051	0.067	0.061	0.040	0.044	—	—	—	—
13 <i>E. sericellum</i>	0.047	0.042	0.035	0.053	0.044	0.038	0.044	0.069	0.052	0.041	0.060	0.041	—	—	—
14 <i>E. gasteromycetoides</i>	0.049	0.043	0.042	0.061	0.048	0.039	0.039	0.069	0.057	0.042	0.060	0.041	0.030	—	—
15 <i>C. dealbata</i>	0.078	0.068	0.074	0.081	0.077	0.071	0.071	0.103	0.081	0.065	0.087	0.066	0.055	0.045	—

cuboid spores (Noordeloos 2012). However, according to Karstedt & al. (2019), *E. calongei* is closer to *Entoloma asterosporum* (Coker & Crouch) T.J. Baroni & Matheny [= *Richoniella asterospora*]. These three species form one of many independent clades of *Entoloma* species possessing cuboid spores (Karstedt & al. 2019). However, the three differ from the others in having a special “pseudocuboid” spore-shape (Karstedt & al. 2019). Co-David & al. (2009) and Karstedt & al. (2019) place these species basal to the Inocephalus–Cyanula superclade, with weak support.

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Xerula setulosa, a new Neotropical agaric record for Argentina

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ABSTRACT—A collection of *Xerula setulosa* is recorded for the first time from Argentina. This species was previously reported from Central America and Brazil. A complete description of the specimens, photographs in the natural habitat, and illustrations of diagnostic microscopic characters are presented. Comments regarding the distribution and related species are provided.

KEY WORDS—*Agaricales*, fungi, mushroom, *Physalacriaceae*, taxonomy

Introduction

Maire (1933) proposed *Xerula* to accommodate *Agaricus longipes* Bull. [= *Xerula pudens* (Pers.) Singer]. The genus has undergone many successive taxonomic reclassifications including genus, subgenus, and section, but always associated in some way with the genera *Oudemansiella* Speg. and *Mucidula* Pat. (Moser 1955; Singer 1962a,b, 1964, 1986; Cléménçon 1979; Dörfelt 1979; Pegler & Young 1987; Halling & Mueller 1999; Petersen 2008; Yang & al. 2009). Morphological and molecular phylogenetic analyses now support *Xerula* as an independent genus within *Physalacriaceae* (Binder & al. 2006, Petersen & Hughes 2010).

Xerula is characterized by its collybioid basidiomata with dark colors (gray, brown to black); white distant and broad lamellae; rooting stipe, with

velutinous, strigose or hispid surface and presence of cauloseae; white spore-print; and hyaline, broadly ellipsoid to globose spores (Wang & al. 2008). *Xerula* is related with *Paraxerula* R.H. Petersen, *Protoxerula* R.H. Petersen, and *Hymenopellis* R.H. Petersen, differing from these in the thick-walled, stiff, brittle, blond to rufous brown pileocystidia (Petersen & Hughes 2010).

There are no previous Argentinean records of species currently accepted in *Xerula*. *Xerula radicata* (Relhan) Dörfelt, which was recorded from Argentina (Niveiro & Albertó 2012; Raithelhuber 1974, 1987, 1991, 1995; Singer 1964; Singer & Digilio 1952), is currently accepted as *Hymenopellis radicata* (Relhan) R.H. Petersen (Petersen & Hughes 2010). The aim of this work is to describe the first Argentinean *Xerula* collection.

Materials & methods

The material, which was collected in the province of Salta, Argentina, was photographed and described macroscopically in situ. The specimens were identified through morphological examination following Largent (1986), Vellinga (1988), and Lodge & al. (2004). Color terminology is according to Kornerup & Wanscher (1978). Specimens were sectioned by freehand and mounted in 5% KOH (v/w) with 1% phloxine aqueous solution for microscopical examination. Melzer's reagent (Wright & Albertó 2002) was used to verify amyloid reaction. Microscopic structures were measured directly with 1000× immersion objective or through photographs taken with a Leica EC3 built-in camera using Image Pro Plus® 4.0 software. The minimum-maximum intervals were provided for the different microscopic structures. For basidiospores, n = number of spores measured, $\bar{x}$ = mean values, Q = length/diameter coefficient, and $Q\bar{x}$ = mean value of Q . Authors of scientific names follow Index Fungorum (2019), and herbarium acronyms follow Thiers (2019). The collection was dried, kept in the freezer for a week, and deposited as reference in the CTES herbarium.

Taxonomy

Xerula setulosa (Murrill) R.H. Petersen & T.J. Baroni,

Mycotaxon 101: 114. 2007.

FIGS 1, 2

≡ *Gymnopus setulosus* Murrill, N. Amer. Fl. 9: 373. 1916.

= *Lentinus pilosus* Rick, Lilloa 2: 310. 1938, nom. illegit. [non (Fr.) Fr. 1838].

≡ *Xerula pilosa* Singer, Lilloa 26: 86. 1954.

≡ *Oudemansiella pilosa* (Singer) Singer, Sydowia 15: 59. 1962.

BASIDIOMATA collybioid, solitary, radicating, growing on humus. PILEUS ≤35 mm diam., convex to depressed plane, with a truncate to mammillate umbo, surface dry, roughened, sometimes delicately arched, on the disc light brown (5D5), pale yellow (4A3) and greyish yellow (4C4), or yellowish

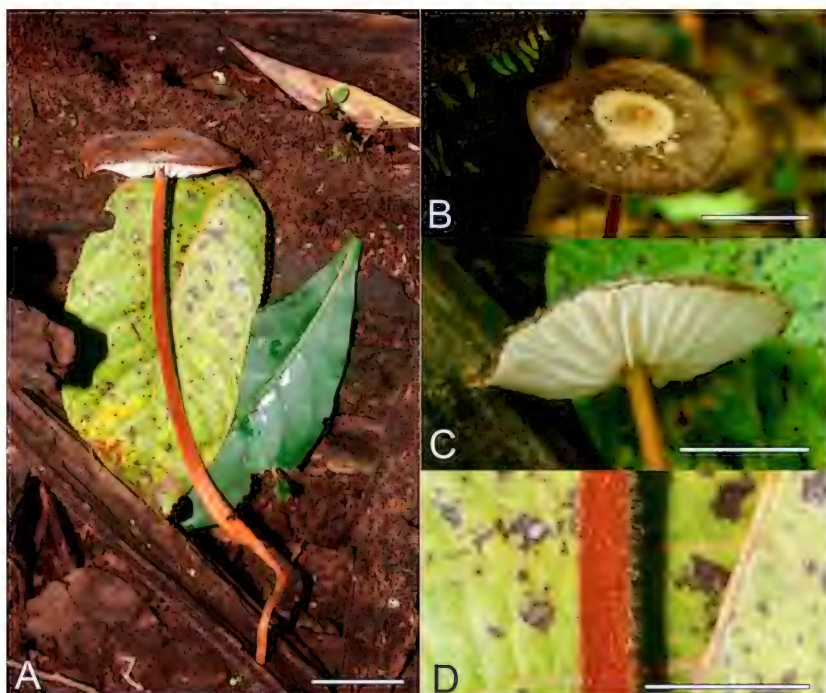


FIG. 1. *Xerula setulosa* (CTES – Niveiro & al. 2198) A. General aspect of basidiomata; B. Detail of pileus; C. Detail of lamellae; D. Detail of stipe pubescence. Scale bars = 20 mm. Photographs by N. Niveiro.

brown (5D6), towards the margin olive brown (5E5) to dark brown (6F5), strongly pubescent with brown hairs, margin somewhat incurved, undulated, not striate. CONTEXT fleshy but very thin, <1 mm, white, unchanging when cut. Smell and taste not checked. LAMELLAE distant to subdistant, white (1A1), adnexed to adnate, ventricose, margin entire, lamellulae two-tiered. STIPE central, $150 \times 4\text{--}8$ mm, compressed, attenuated base and apex, hollow, grayish orange (6B6) to brownish orange (7C8), strongly pubescent, hairs ≤ 1 mm, greyish-yellow (4B4) to golden (4C6); leathery pseudorhiza attenuating quickly, stipe concolorous with the stipe, pubescent. ANNULUS and other velar structures absent. SPORE-PRINT white (1A1).

BASIDIOSPORES $10\text{--}13.8 \times 10\text{--}12.5$ μm ; $x = 12.2 \times 11$ μm ; $Q = 0.97\text{--}1.3$; $Qx = 1.1$; $n = 25$; globose to subglobose, thin-walled, smooth, chestnut, lacking evident germ pore, with a prominent apiculus. BASIDIA 30–60

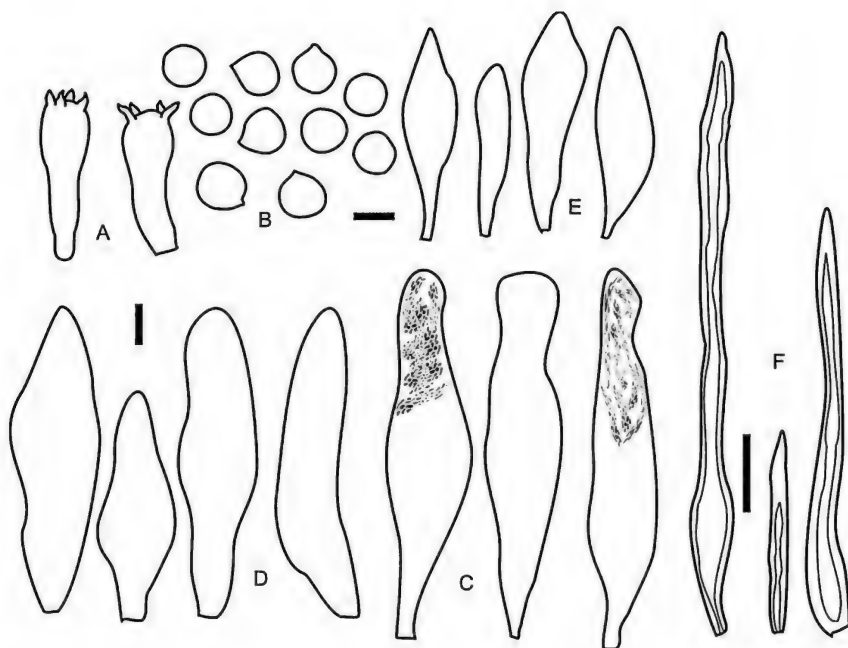


FIG. 2. *Xerula setulosa* (CTES – Niveiro & al. 2198): A. Basidia; B. Spores; C. Cheilocystidia; D. Pleurocystidia; E. Pileipellis elements; F. Pileipellis pileosetae.
Scale bars: A–D = 10 µm, F = 40 µm.

× 10–17 µm, claviform to ventricose, 4-spored, thin-walled, hyaline. PLEUROCYSTIDIA 60–130 × 12–35 µm, broadly lageniform, with a truncate apex, thin to thick-walled mainly at the base. CHEILOCYSTIDIA 50–80 × 10–24 µm, fusiform to utriform, thin-walled to thickened at the base, hyaline. HYMENOPHORAL TRAMA bilateral with a thin half-layer and divergent gelatinous hyphae. PILEIPELLIS hymeniform, composed of two types of elements: 1) Pileocystidia fusiform, 45–60 × 15–18 µm, thick-walled, pigmented with olive content; 2) Pileosetae ≤ 700 µm long, 10–17 µm diam., dark brown with sharp ends and thickened (≤ 4 µm) walls. Stipe surface composed of two elements, similar to the pileocystidia and pileosetae. CLAMP CONNECTIONS absent.

SPECIMEN EXAMINED—ARGENTINA. SALTA PROVINCE. Santa Victoria Dept., Baritú National Park, road to Baritú town, 22°26'41"S 64°44'37"W, 1421 m a.s.l., 22.III.2011, leg. Niveiro & al. 2198 (CTES).

Discussion

Xerula setulosa is characterized by its strongly pubescent basidioma, yellowish brown to dark brown pileus surface, orange brown stipe, pure white lamellae, globose smooth spores, and numerous cystidia (Wang & al. 2008). It was originally described from Brazil by Rick (1938) under the illegitimate name *Lentinus pilosus* [$\equiv$ *Xerula pilosa* (Singer 1954); $\equiv$ *Oudemansiella pilosa* (Singer 1962b)]; however, Petersen & Baroni (2007) synonymized these names under *Xerula setulosa*.

The only *Xerula* species previously reported from Argentina (as *X. radicata*) is currently named as *Hymenopellis radicata*, which differs morphologically from *X. setulosa* by the absence of pubescence (Putzke & Pereira 1988, Raithelhuber 1995).

Six species are currently accepted in *Xerula*: *X. hispida* Halling & G.M. Muell., *X. melanotricha* Dörfelt, *X. pudens*, *X. setulosa*, *X. sinopudens* R.H. Petersen & Nagas., and *X. strigosa* Zhu L. Yang & al. They can be distinguished by basidiome color, basidiospore morphology, setae, and other microscopic characters (Wang & al. 2008, Petersen & Hughes 2010). Distribution is also significant in that species are generally limited to certain geographical areas; so far, species reported from Europe and Asia are not found in the Americas.

Xerula setulosa seems closely related to *X. hispida* because of its strongly pubescent basidioma and the presence of a pseudorhiza (Petersen & Baroni 2007, Rodríguez-Alcántar & Herrera-Fonseca 2016). However, *X. hispida* is distinguished by microscopic characters, such as bisporic basidia and the presence of clamp connections. Petersen & Baroni (2007) hypothesized that *X. hispida* might represent an asexual state of *X. setulosa*, but unpublished molecular studies by Wang & al. (2008) placed the two species in different clades. On the other hand, Halling & Mueller (1999) reported absence of clamp connections in *X. hispida*. Both species have a similar distribution in Mexico, Central America, and South America.

Xerula melanotricha is clearly separated by its distribution (Europe, western Asia and northern Africa) and the presence of its very long, almost black setae ≤ 3 mm that are usually visible to the naked eye. However, in some younger *X. melanotricha* specimens possess hairs that barely exceed 1 mm; these can be difficult to measure, especially hairs on the cap of dried herbarium material which are often broken (Ronikier 2003).

Xerula pudens (the current name of the generic type *Agaricus longipes* Bull.) is widely distributed throughout Europe and in southwestern Russia;

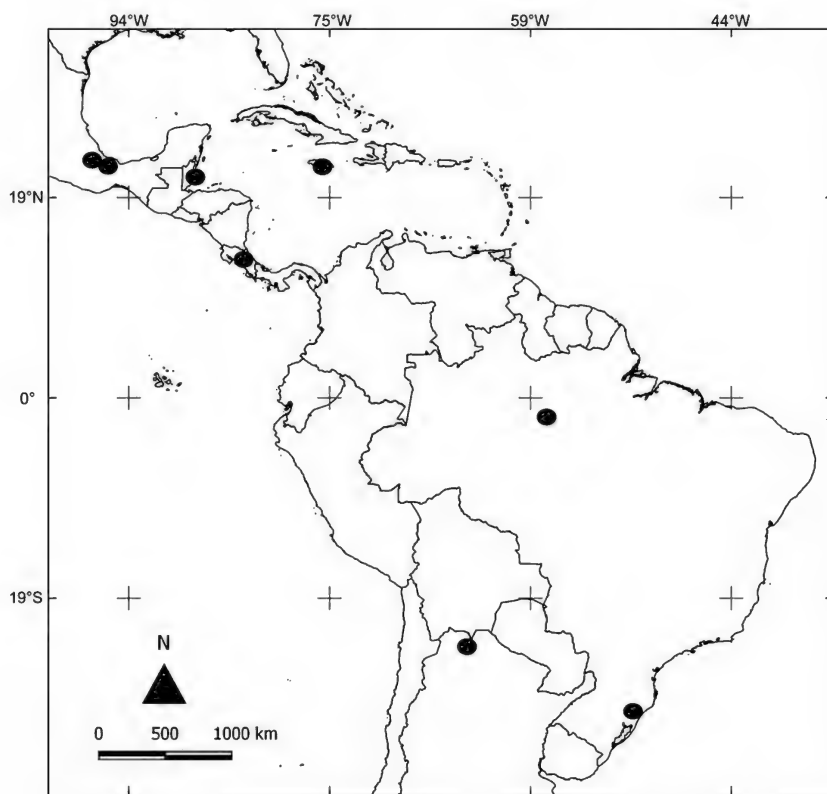


FIG. 3. Distribution of *Xerula setulosa* in America. Map adapted by N. Niveiro.

it is distinguished from *X. setulosa* by its longer basidioma with a small pileus in relation to the stipe.

Xerula sinopudens, distributed in tropical to temperate Asia, is characterized by its carrot-shaped pseudorhiza and interspersed long (0.55 mm) and short pileosetae (Petersen & Hughes 2010).

Xerula strigosa of southwest China and Southeast Asia, which is macroscopically remarkably similar to *X. setulosa*, can be distinguished with difficulty microscopically by its longer ($11\text{--}5 \times 9\text{--}11.5 \mu\text{m}$) basidiospores, occasional clamp connections on the septa of basidia and lamellar hyphae, and thin-walled pleurocystidial apices (Wang & al. 2008).

As regards pileus size, our material differs from previous descriptions. The pileus is larger (35 mm) than those reported by Putzke & Pereira (1988; ≤ 10 mm) and Petersen & Baroni (2007; ≤ 20 mm), although it is close to or matches material from Paraná, Brazil (23–40 mm; Meijer 2008) and Jalisco, Mexico (20–30 mm; Rodríguez-Alcántar & Herrera-Fonseca 2016). Our Argentinean basidiospore size is similar to those in Meijer (2008) and Petersen and Baroni (2007), larger than in Singer (1954, 1964; $10 \times 6.9 \mu\text{m}$) and smaller than in Dörfelt (1985; $10\text{--}16 \times 9.5\text{--}14 \mu\text{m}$) and Wang (2008; $11\text{--}16 \times 9.5\text{--}12 \mu\text{m}$). Taking into account pileus colour and size, the spores, the pleurocystidia, and the caulocystidia size, the Argentinean specimen described here matches the descriptions by Meijer (2008) and Rodríguez-Alcántar & Herrera-Fonseca (2016).

Xerula setulosa has a Neotropical distribution (FIG. 3) and has been reported from Mexico, Belize, Jamaica, Puerto Rico (Petersen & Baroni 2007), Brazil (Putzke & Pereira 1988, Meijer 2002, 2006, 2008), and Costa Rica (Wang & al 2008). The present record represents the first report from Argentina.

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Haematomma rubidum sp. nov. from China

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ABSTRACT—*Haematomma rubidum* from southern China is described as new species characterized by convex apothecia with thin whitish margins that become hidden in age; submuriform ascospores with 15–21 transverse and 0–3 longitudinal septa; and a thallus containing atranorin and russulone but lacking dibenzofurans or xanthenes. Photographs of the new species accompany a detailed taxonomic description.

KEYWORDS—East Asia, *Haematommataceae*, lichenized fungi, taxonomy

Introduction

Haematomma A. Massal. is a cosmopolitan genus characterized by blood-red lecanorine apothecia and transversely septate, submuriform to muriform ascospores. Three species that produce submuriform spores are *H. parda* Aptroot, *H. staigeriae* Nelsen & al., and *H. wattii* (Stirt.) Zahlbr. (Staiger & Kalb 1995, Nelsen & al. 2006, Aptroot 2007), while only one, *H. gallowayi* Brodo, is characterized by muriform spores (Brodo 2007).

During our studies, we discovered a new *Haematomma* species in Yunnan Province (21°08'–29°15'N, 97°31'–106°12'E) in southwestern China. The natural conditions and dry and wet climate in the province provide excellent

[#] RONG TANG & AN-CHENG YIN contributed equally to this research.

habitat for many rare species and Yunnan is the most species-rich region for lichens in China (Wang 2012).

Here we describe a new submuriform-spored species of *Haematomma* and present a brief diagnosis, together with discussion on the differences between (sub)muriform-spored species of *Haematomma*.

Materials & methods

The voucher specimens were examined morphologically using an Olympus SZ51 stereomicroscope and Olympus CX21 polarizing microscope and photographed with Olympus SZX16 and BX61 with DP72 cameras. Both thallus and medulla were tested with K (a 10% aqueous solution of potassium hydroxide) and C (a saturated solution of aqueous sodium hypochlorite). Lichen substances were identified using standardized thin layer chromatography techniques (TLC) with solvent systems A and C (Orange & al. 2010). The collection is deposited in the lichen section of the Herbarium, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China (KUN).

Taxonomic description

Haematomma rubidum R. Tang & Z.T. Zhao, sp. nov.

FIG. 1

MB 835897

Differs from *Haematomma staigeriae* by its convex apothecia, its lack of soralia, and the absence of lichexanthone.

TYPE: China. Yunnan Province, Lijiang City, Mt. Maanshan, Jiushijiulongtan Lake, 26°39'N, 99°46'E, alt. 3400 m, on *Rhododendron*, 16 Aug. 2000, LS Wang 00–20099 (Holotype, KUN).

ETYMOLOGY: *rubidum* refers to both the red *Rhododendron* blooms of its substrate and the red disc of the lichen.

THALLUS crustose, corticolous, smooth, slightly cracked, without isidia or soralia, whitish, thin, 0.05 mm thick; prothallus not seen. APOTHECIA 0.5–1.0 mm diam., constricted at the base, dispersed, disc cinnabar-red to brownish-red, primarily plane, soon becoming convex, epruinose, margin thin, initially flush with disk but soon becoming hidden with age; AMPHITHECIUM 75–95 µm thick; EPIHYMENIUM orange-red, K+ red, 5–7.5(–10) µm thick; HYMENIUM hyaline, 75–90 µm tall; HYPOTHECIUM hyaline or slightly brown; PARAPHYSES branched and anastomosing. ASCI clavate, containing 8 spores; ASCOSPORES persistently colorless, fusiform, submuriform with 15–21 transverse and 0–3 longitudinal septa per segment in optical view, 75–100 × 10–12.5 µm, the last cell of the spore, 20–25 µm long. The upper half of some spores muriform, while the lower half transversely septate. PYCNIDIA: not observed.

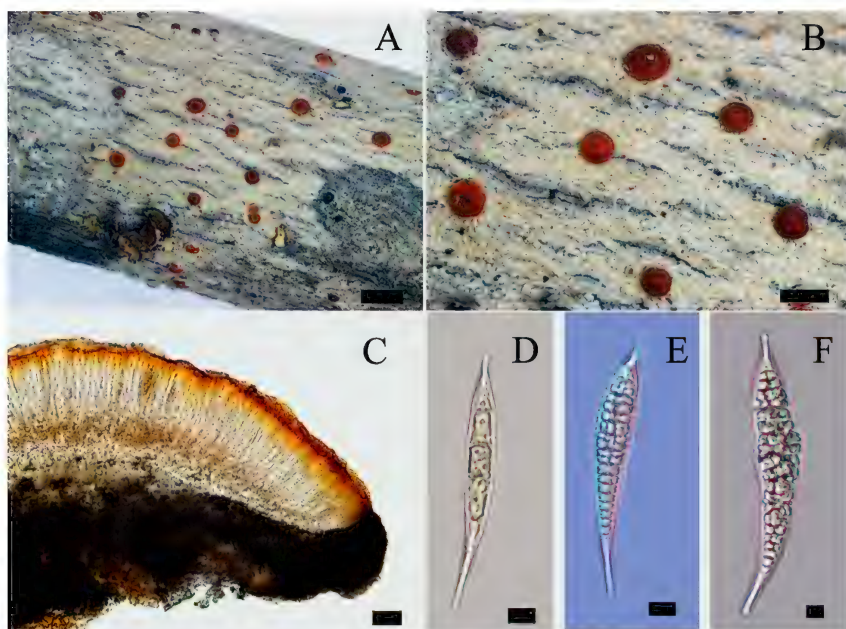


FIG.1: *Haematomma rubidum* (holotype, KUN 00–20099). A. Thallus; B. Thallus with apothecia; C. Section through apothecium; D–F. Ascospores. Scale bars: A = 2 mm; B = 1 mm; C = 50 μ m; D, E = 10 μ m; F = 5 μ m.

CHEMISTRY—Cortex and medulla K+ yellow, C–, KC–, IKI–. Atranorin and russulone detected by TLC.

HABITAT—Growing with *Lecidella* spp. on the trunk of *Rhododendron* on a sunny slope, above 3000 m elevation.

COMMENTS—*Haematomma rubidum* is characterized by its convex apothecia, submuriform ascospores, and K+ red epihymenium. When young the apothecial margin is usually even with disk but eventually becomes hidden or covered in the lower part due to the gradual bulging of disk. *Haematomma* identification is still based on classical taxonomy. Nonetheless, its unique morphology and chemistry significantly separate *H. rubidum* from other *Haematomma* species. These differences support our proposing a single collection as a new species, but future DNA sequence analyses are needed to confirm its taxonomic disposition.

Haematomma staigeriae, which also possesses submuriform spores and a K+ red epihymenium, can be distinguished by its narrower (6–10 μ m)

TABLE 1. Distinguishing characteristics of (sub)muriform-spored *Haematomma* species

CHARACTER	<i>H. rubidum</i>	<i>H. gallowayi</i>	<i>H. parda</i>	<i>H. staigeriae</i>	<i>H. wattii</i>
SORALIA	Absent	Present	Partly present	Present	Absent
APOTHECIUM					
Disc	Cinnabar- to brownish-red, convex	Cinnabar red, smooth	Brown, flat	Cinnabar-red, smooth	Cinnabar- red, smooth
Margin	Thin	Thick	Thick	Thick	Thick
EPIHYMENIUM	K+ red	K+ purple	K–	K+ red	K+ purple
ASCOSPORE					
Type	Submuriform	Muriform	Submuriform	Submuriform	Submuriform
Long. septa	0–3	1–3	0–2	0–1	0–1
Transverse septa	15–21	(6–)12–17 (–23)	14–17	11–23	15–25
Length (µm)	75–100 ×	(46–)51–78 ×	55–75 ×	50–90 ×	60–95 ×
Width (µm)	10–12.5	10–15.5	5–7.5	6–10	6.5–10
CHEMISTRY					
Atranorin	+	+	+	+	+
Haematommone	—	+	—	—	+
Lichexanthone	—	—	—	+	—
Placodiolic acid	—	+	—	—	+
Russulone	+	—	—	+	—
Zeorin	—	+	—	—	—
Unk. substance	—	—	+ (2)	+	—
REFERENCE	This study	Brodo 2007	Aptroot 2007	Nelsen & al. 2006	Staiger & Kalb 1995

ascospores, flat discs, and a thallus with soralia and lichexanthone. In China, another species of *Haematomma* with submuriform spores, *H. wattii*, has been reported. However, *H. wattii* contains haematommone rather than russulone. The main differences among (sub)muriform-spored species of *Haematomma* are shown in TABLE 1.

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***Armillaria xiaocaobaensis* sp. nov. from China**

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ABSTRACT—A new wood-inhabiting fungal species from Yunnan Province, China, is proposed based on morphological and molecular characters. *Armillaria xiaocaobaensis* is characterized by a central stipe, striate to furrowed orange yellow to pinkish brown pileus surface, membranous annulus, and ellipsoid, a monomitic hyphal system with generative hyphae bearing simple septa, and slightly thick-walled basidiospores averaging $7.7 \times 4.9 \mu\text{m}$. TEF1 sequence analyses support *A. xiaocaobaensis* as a distinct taxon in *Armillaria*.

KEY WORDS—*Agaricales*, phylogenetic, *Physalacriaceae*, pathogenic fungi, taxonomy

Introduction

Species in *Armillaria* (Fr.) Staude (*Physalacriaceae*, *Basidiomycota*) are well known as important plant pathogens that can cause serious root diseases on diverse trees and woody plants, resulting in huge economic losses (Wargo & Shaw 1985, Baumgartner 2004, Lalande & al. 2018).

Armillaria includes approximately 40 species (Volk & Burdsall 1995, Kirk & al. 2008, Brazeel & al. 2012, Hood & Ramsfield 2016, Elías-Román & al. 2018) worldwide, and ten *Armillaria* species are currently recognized in China (Qin & al. 2000, 2007; Sun & al. 2003; Zhao & al. 2008; Coetzee & al. 2015; Guo & al. 2016).

Recent phylogenetic studies of *Armillaria* based on sequences of the internal transcribed spacer (ITS) region, the large subunit of nuclear

ribosomal RNA gene (nLSU), translation elongation factor 1- α (TEF1), and β -tubulin have greatly increased the number of identified fungal species and revealed the relationships among species in this genus (e.g., Maphosa & al. 2006, Hasegawa & al. 2010, Ross-Davis & al. 2012, Tsykun & al. 2013, Coetzee & al. 2015, Park & al. 2018). Lima & al. (2008) described one new South American species, *Armillaria paulensis* Capelari, based on morphology and ITS sequences that showed its closeness to *A. luteobubalina* Watling & Kile, while Brazee & al. (2012) introduced *A. altimontana* Brazee & al. in North America based on morphological and molecular phylogenetic evidence. In New Zealand, Hood & Ramsfield (2016) revealed *A. aotearoa* I.A. Hood & Ramsfield using morphology, interfertility cultures, and DNA sequence data. Guo & al. (2016) analyzed Chinese *Armillaria* samples using the sequences of ITS, TEF1 and β -tubulin gene, which revealed 15 phylogenetic lineages of *Armillaria* from China and showed that TEF1 was the most parsimony informative. Koch & al. (2017) resolved phylogeny and biogeography of *Armillaria*, *Desarmillaria* (Herink) R.A. Koch & Aime, and *Guyanagaster* T.W. Henkel & al. Elías-Román & al. (2018) described *A. mexicana* Elías-Román & al. based on morphology, DNA-sequence data (ITS, nLSU and TEF1), and phylogenetic analyses.

Our research on macrofungi in southern China revealed specimens that could not be assigned to any described species within *Armillaria*. The authors sampled previous research using the translation elongation factor-1 alpha gene (TEF1) sequences to explore the taxonomy and phylogeny of this undescribed species, proposed below as *Armillaria xiaocaobaensis*.

Materials & methods

Macroscopical descriptions were based on field notes. Color terms follow Petersen (1996). Dried material was examined microscopically using a compound microscope following Dai (2012). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = cotton blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both inamyloid and nondextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens. The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC).

Genomic DNA was extracted from dried specimens using the EZNA HP Fungal DNA Kit according to the manufacturer's instructions with some modifications. A small piece (about 30 mg) of dried fungal specimen was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 mL centrifuge tube, suspended

in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min. After 0.4 mL phenol-chloroform (24:1) was added to the tube, the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with 0.45 mL binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 100 mL elution buffer was added to the middle of adsorbed film to elute the genomic DNA. TEF1 was amplified with primer pairs EF1-983F and EF1-2218R (Rehner 2001). The PCR procedure for TEF1 was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 59 °C for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited in GenBank (TABLE 1).

GeneCodes Sequencer 4.6 was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 (<https://mafft.cbrc.jp/alignment/server/index.html>) using the “G-INS-I” strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 24610). *Oudemansiella cubensis* (Berk. & M.A. Curtis) R.H. Petersen and *Strobilurus esculentus* (Wulfen) Singer were used as outgroup to root trees following Koch & al. (2017) in the TEF1 analyses.

Phylogenetic analyses of the TEF1 sequences were performed using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated. Sequences were analyzed using Maximum Likelihood (ML) with RAXML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations (TEF1) and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority

TABLE 1. Sequences used in the phylogenetic analyses; new sequences in **bold**.

SPECIES	SAMPLE NO.	GENBANK NO. TEF1	REFERENCE
<i>Armillaria altimontana</i>	D 82	JN944611	Brazee & al. 2012
	POR 100	JN944606	Brazee & al. 2012
<i>A. aotearoa</i>	NZFRIM 5283	KU295542	Hood & Ramsfield 2016
<i>A. borealis</i>	HKAS 56108	KT822293	Guo & al. 2016
	HKAS 76263	KT822294	Guo & al. 2016
<i>A. calvescens</i>	ST 17	JF895836	Brazee & al. 2011
	ST 18	JF895837	Brazee & al. 2011
	ST 3	JF895835	Brazee & al. 2011
<i>A. cepistipes</i>	F 011081	KT822416	Guo & al. 2016
	S 20	JF313116	Brazee & al. 2011
<i>A. fumosa</i>	CMW 4955	DQ435646	Maphosa & al. 2006
<i>A. fuscipes</i>	CMW 3164	DQ435621	Maphosa & al. 2006
	CMW 4953	DQ435622	Maphosa & al. 2006
<i>A. gallica</i>	M 70	HQ432899	Direct Submission
	ST 22	HQ432897	Elías-Román & al. 2018
<i>A. gemina</i>	ST 8	JF313136	Brazee & al. 2011
	ST11A	JF313133	Brazee & al. 2011
<i>A. heimii</i>	K 59	FJ618644	Elías-Román & al. 2018
	PH 8724	FJ618651	Elías-Román & al. 2018
<i>A. hinnulea</i>	CMW 4980	DQ435648	Maphosa& al. 2006
<i>A. limonea</i>	CMW 4680	DQ435655	Maphosa& al. 2006
	CMW 4991	DQ435656	Maphosa & al. 2006
	Plim 8466	FJ618654	Elías-Román & al. 2018
<i>A. luteobubalina</i>	CMW 4977	DQ435657	Maphosa & al. 2006
	CMW 8876	DQ435658	Maphosa & al. 2006
<i>A. mellea</i>	CMW 4613	DQ435637	Maphosa & al. 2006
	G 0405414	KT822345	Guo & al. 2016
	MEX 74	KC111011	Elías-Román & al. 2018
<i>A. mexicana</i>	MEX 85	KR061313	Elías-Román & al. 2018
	MEX 87	KR061314	Elías-Román & al. 2018
	MEX 88	KR061315	Elías-Román & al. 2018
<i>A. nabsnona</i>	C 21	JF313119	Elías-Román & al. 2018
	HKAS 85523	KT822411	Guo & al. 2016
<i>A. novae-zelandiae</i>	CMW 4722	DQ435652	Maphosa & al. 2006
	CMW 5448	DQ435653	Maphosa & al. 2006
<i>A. ostoyae</i>	EC4	JF746925	Brazee & al. 2011
	EC 5	JF746926	Brazee & al. 2011
<i>A. pallidula</i>	3626	FJ618665	Elías-Román & al. 2018
	CMW 4971	DQ435647	Maphosa & al. 2006
<i>A. puiggarii</i>	MCA 3111	KU289104	Koch & al. 2017
	TH 9751	KU289113	Koch & al. 2017

SPECIES	SAMPLE NO.	GENBANK NO. TEF1	REFERENCE
<i>A. sinapina</i>	A 9601539	KT822422	Guo & al. 2016
	M 50	JF313114	Brazee & al. 2011
	ST 12	JF313132	Brazee & al. 2011
	ST 13	JF313131	Brazee & al. 2011
<i>A. solidipes</i>	P 1404	JF313140	Brazee & al. 2011
	ST 2	JF313139	Brazee & al. 2011
<i>A. xiaocaobaensis</i>	SWFC 12637	MN298777	This study
	SWFC 12638[T]	MN298778	This study
	SWFC 12639	MN298779	This study
<i>Desarmillaria ectypa</i>	7001113	KT822438	Guo & al. 2016
	CMW 15693	FJ875698	Koch & al. 2017
	MY 84941	FJ618643	Koch & al. 2017
<i>D. tabescens</i>	90158	KT822439	Koch & al. 2017
	I 9912213	KT822441	Guo & al. 2016
	PT 8412	FJ618658	Koch & al. 2017
<i>Guyanagaster necrorhizus</i>	G 314	KU289110	Koch & al. 2017
	G 352	KU289109	Koch & al. 2017
	MCA 3950	KU289107	Koch & al. 2017
	RAK 31	KU289108	Koch & al. 2017
<i>Oudemansiella cubensis</i>	MCA 5434	KU289105	Koch & al. 2017
<i>Strobilurus esculentus</i>	Yang 5027	KF530581	Koch & al. 2017

rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BT), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BS, BT) and 0.95 (BPP) were considered significantly supported.

Molecular phylogeny

The TEF1 dataset included sequences from 62 fungal specimens representing 29 species (TABLE 1). The alignment comprised 544 characters of which 312 characters were constant, 29 variable and parsimony-uninformative, and 203 parsimony-informative. Maximum parsimony analysis yielded four equally parsimonious trees (TL = 728, CI = 0.496, HI = 0.504, RI = 0.781, RC = 0.387). Best model for the TEF1 dataset estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.003738 (BI).

The phylogeny inferred from TEF1 sequences placed *Armillaria xiaocaobaensis* in a monophyletic lineage with strong support (BS = 100%; BT = 100%; BPP = 1).

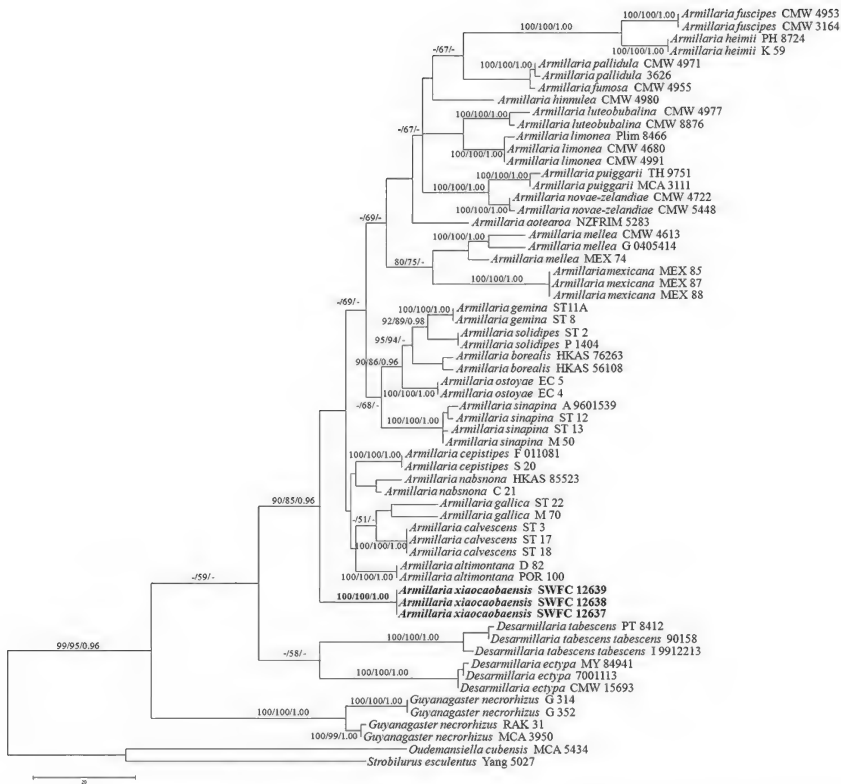


Fig. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Armillaria xiaocaobaensis* and related species based on TEF1 sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50%, and Bayesian posterior probabilities >0.95.

Taxonomy

Armillaria xiaocaobaensis Jia H. Peng & C.L. Zhao, sp. nov.

FIGS 2, 3

MB 832231

Differs from *Armillaria altimontana* by its centrally stipitate basidiomes with striate to furrowed, orange yellow to pinkish brown pileus surface, membranous annulus, and smaller, ellipsoid, thin-walled basidiospores.

TYPE: China. Yunnan Province: Zhaotong, Yiliang County, Xiaocaoba Town, on angiosperm trunk, 19 April 2019, Jia-Hua Peng (Holotype, SWFC 0012638; GenBank MN298777).

ETYMOLOGY: *xiaocaobaensis* (Lat.) refers to the locality (Xiaocaoba Town) of the type specimen.



FIG. 2. *Armillaria xiaocaobaensis* (holotype, SWFC 0012638).

Scale bars: A = 4 cm; B, C = 1 cm; D = 5 mm; E = 2 mm.

BASIDIOMATA pileate, centrally stipitate, caespitose. PILEUS 30–40 mm diam., umbonate, convex to plano-convex, orbicular in apical view, margin deflexed to lobed, pileus surface striate to furrowed, orange yellow to pinkish brown in the center, and pale yellow to pale brown at margin. LAMELLAE 5 mm deep, close,

decurrent, adnate, edges entire, buff to light yellow. LAMELLULAE attenuate, edges entire, multi-tiered. ANNULUS 4–5 mm wide, superior, persistent, membranous, appressed to stipe, buff to light yellow. STIPE 35–60 × 4–6 mm, central, cylindrical, solid, light yellow to pale pinkish brown to brown to black toward the base in fresh specimens, base bulbous. RHIZOMORPHS absent. TASTE AND ODOR not tested. SPORE PRINT white.

BASIDIOSPORES ellipsoid, hyaline, slightly thick-walled, smooth, IKI–, CB–, (6.5–)7–8.5(–9) × 4–5.5(–6) μm , $L = 7.74 \mu\text{m}$, $W = 4.93 \mu\text{m}$, $Q = 1.53\text{--}1.64$ ($n = 90/3$). BASIDIA barrel-shaped to clavate, with 2–4 sterigmata and a simple basal septum, 20–28 × 5.5–8.5 μm ; basidioles dominant, mostly clavate but slightly smaller than basidia. HYMENOPHORAL TRAMA generative hyphae bearing simple septa, hyaline, thin-walled, unbranched, 5–8 μm in diam. CYSTIDIA none observed. PILEIPELLIS hyphae hyaline, thin-walled, unbranched, 8–13 μm diam. CONTEXT 100–150 μm wide, hyphae hyaline, thin-walled, unbranched, 6–10 μm diam. STIPITPELLIS hyphae hyaline, thin-walled, unbranched, 3.5–5.5 μm diam. CLAMP CONNECTIONS absent.

ADDITIONAL SPECIMENS EXAMINED: CHINA. YUNNAN PROVINCE. Zhaotong: Yiliang County, Xiaocaoba Town, on angiosperm trunk, 19 June 2019, Jia-Hua Peng (SWFC 0012637; SWFC 0012639).

Discussion

Phylogenetic analyses and morphological characters support *Armillaria xiaocaobaensis* as a new species.

In the TEF1 analyses (FIG. 1), *A. xiaocaobaensis* formed a monophyletic lineage with strong support (BS = 100%; BT = 100%; BPP = 1) and grouped with *Armillaria altimontana*, *A. calvescens* Bérubé & Dessur., *A. cepistipes* Velen., *A. gallica* Marxm. & Romagn., and *A. nabsnona* T.J. Volk & Burds. However, morphologically *A. altimontana* differs from *A. xiaocaobaensis* by its tricholomatoid basidiomata with a reddish brown pileus bearing cream scales and short fibrils (Brazee & al. 2012) and from *A. calvescens* by the presence of pileus scales and fibrils, and larger basidiospores (8.5–10 × 5–7 μm ; Bérubé & Dessureault 1989). *Armillaria cepistipes* differs in its yellow ochraceous to ochraceous brown pileus, longer stipe (100 × 9–11 mm), and larger basidia (29–45 × 8.5–11 μm ; Antonín & al. 2009); and *A. gallica* by the presence of dark brown to pinkish brown pileus, long fibrillose pileus scales, and ellipsoid to amygdaloid, larger basidiospores (7.5–11 × 5–6.5 μm ; Antonín & al. 2009). *Armillaria nabsnona* has a hygrophanous pileus with a white context and larger basidiospores (8–10 × 5.5–6.5 μm ; Volk & al. 1996).

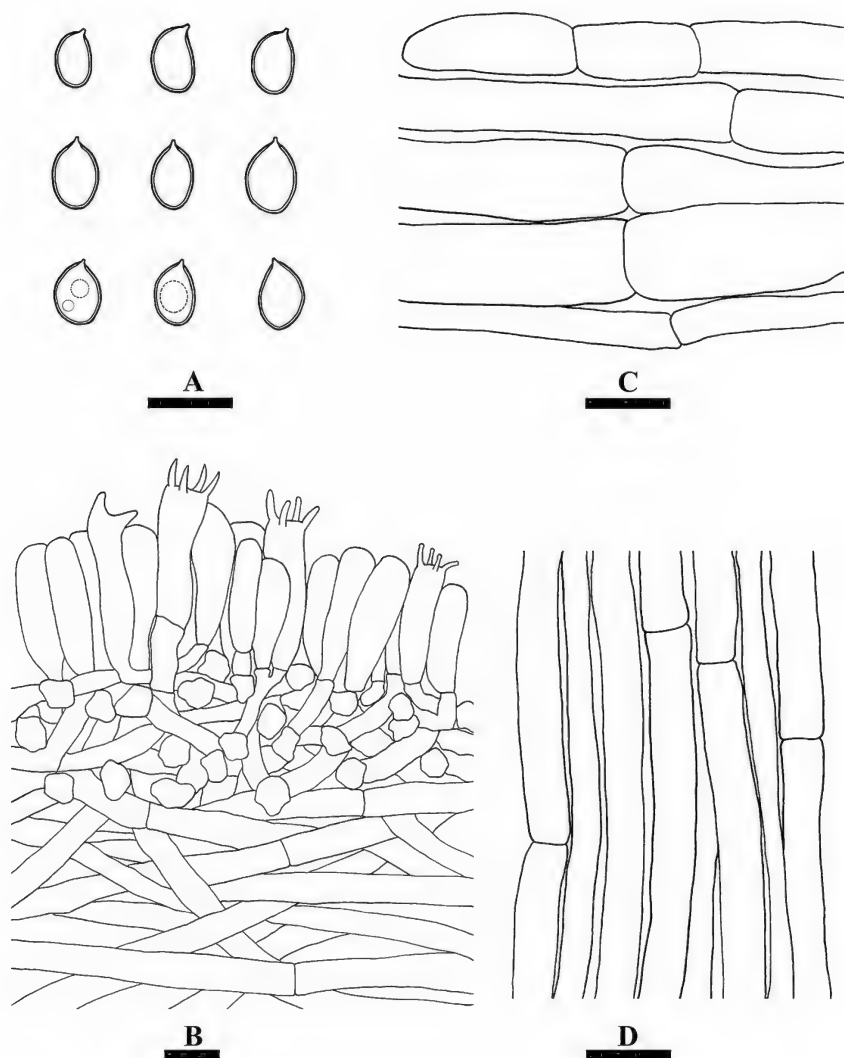


FIG. 3. Microscopic structures of *Armillaria xiaocaobaensis* (drawn from the holotype, SWFC 0012638). A. Basidiospores; B. Section of hymenium; C. Pileipellis; D. Stipitipellis. Scale bars: A–D = 10 μ m.

Armillaria xiaocaobaensis is close to *Desarmillaria*, a member in the sister genus based on the molecular data (FIG. 1). *Desarmillaria* is distinguished morphologically from *Armillaria* by the absence of an annulus (Koch & al. 2017).

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Phylogeny and morphology of *Ellismarsporium parvum* and the new combination *E. varium*

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ABSTRACT—LSU DNA sequence analyses place *Ellismarsporium parvum* in *Pleosporales*. The morphology of the species in pure culture is described and illustrated. *Helminthosporium varium* is recombined as *E. varium*, based on its morphology.

KEY WORDS—*Ascomycota*, asexual fungi, hyphomycetes, phylogeny, taxonomy

Introduction

Ellismarsporium R.F. Castañeda & X.G. Zhang, typified with *E. hypselodelphyos* (M.B. Ellis) R.F. Castañeda & X.G. Zhang is characterized by macronematous and mononematous unbranched conidiophores that

bear integrated and intercalary polytretic conidiogenous cells (Castañeda-Ruiz & al. 2017). The phragmosporic distoseptate conidia are produced in acropetal unbranched or branched chains. Production of conidial chains is the main diagnostic character distinguishing *Ellismarsporium* from *Helminthosporium* Link typified by *H. velutinum* Link. Phylogenetic LSU sequence analysis of strains of *E. parvum* and *Helminthosporium* species has provided additional information on the differences between these genera.

Materials & methods

Pure cultures of *Ellismarsporium parvum* from INIFAT WDCM 853 were transferred to sterilized Petri dishes containing V8 agar (125 ml V8 juice, 18 g agar, 1000 ml distilled water, pH 6.3). Plates were incubated at 25°C in a 12 h dark/light cycle using a box equipped with near UV (black light) VICA FLB-20W T10 lamps. Colony colors were coded according to Rayner (1970). Mounts were prepared in PVL (polyvinyl alcohol, lactic acid) and structures were measured at ×1000 under a Nikon Eclipse Ni-U microscope with bright field optics and photographed using DIC optics with a Nikon DS-Fi2 camera at Universidade Federal de Pernambuco, Recife, Brazil.

TABLE 1. LSU sequences of *Ellismarsporium parvum* and allied species used in the phylogenetic analysis. New sequences are indicated in **bold**.

SPECIES	CULTURE	GENBANK	REFERENCE
<i>Anteaglonium abbreviatum</i>	GKM219N	GQ221881	Mugambi & Huhndorf 2009
<i>A. parvulum</i>	SMH5210	GQ221907	Mugambi & Huhndorf 2009
<i>Clohesyomyces aquaticus</i>	MFLUCC11-0092	JX276950	Zhang & al. 2012
<i>Corynespora cassiicola</i>	C13-1	KF590123	Palomares-Rius & al. 2014
	SK01	LC177365	Chairin & al. 2017
<i>C. pseudocassiicola</i>	CPC 31708	MH327830	Crous & al. 2018
<i>C. smithii</i>	L133 18S	KY984299	Voglmayr & Jaklitsch 2017
<i>C. torulosa</i>	CPC 15989	KF777207	Crous & al. 2013
<i>Ellismarsporium parvum</i>	INIFAT-2457	MN032445	This study
	INIFAT-2483	MN032446	This study
	CBS 190.95	MH874149	Vu & al. 2019
<i>Flavomyces fulophazii</i>	CBS 135761	KP184040	Knapp & al. 2015
<i>Fuscostagonospora cytisi</i>	MFLUCC 16-0622	KY770978	Crous & al. 2018
<i>F. sasae</i>	KT 1467	AB807548	Tanaka & al. 2015
<i>Helminthosporium asterinum</i>	CBS 203.35	MH867156	Vu & al. 2019
<i>H. caespitosum</i>	L151	KY984306	Voglmayr & Jaklitsch 2017
<i>H. dalbergiae</i>	H 4628	AB807521	Tanaka & al. 2015
<i>H. genistae</i>	L144	KY984312	Voglmayr & Jaklitsch 2017
<i>H. leucadendri</i>	CBS 135133	KF251654	Quaedvlieg & al. 2013
<i>H. massarinum</i>	KT 838	AB807523	Tanaka & al. 2015

<i>H. magnisporium</i>	H 4627	AB807522	Tanaka & al. 2015
<i>H. microsorum</i>	L96	KY984329	Voglmayr & Jaklitsch 2017
<i>H. oligosporum</i>	L93	KY984333	Voglmayr & Jaklitsch 2017
<i>H. quercinum</i>	L107	KY984336	Voglmayr & Jaklitsch 2017
<i>Hongkongmyces pedis</i>	HKU 35	NG 056287	Tsang & al. 2014
<i>H. thailandica</i>	MFLUCC 16-0406	KY771321	Crous & al. 2018
<i>Keissleriella cladophila</i>	UTHSC:DI16-326	LN907469	Valenzuela-Lopez & al. 2017
<i>K. culmifida</i>	KT 2308	AB807591	Tanaka & al. 2015
	KT 2642	AB807592	Tanaka & al. 2015
<i>K. gloeospora</i>	KT 829	AB807589	Tanaka & al. 2015
<i>Kirschsteiniothelia aethiops</i>	CBS 111.56	MH869065	Vu & al. 2019
	CBS 118.59	MH877780	Vu & al. 2019
	CBS 111.61	MH869545	Vu & al. 2019
<i>Lentithecium carbonneanum</i>	CBS 144076	MH062991	Crous & al. 2018
<i>L. cloninum</i>	KT 1149A	AB807540	Tanaka & al. 2015
<i>L. lineare</i>	IFRD 2008	FJ795435	Zhang & al. 2009
<i>L. pseudoclioninum</i>	KT 1113	AB807545	Tanaka & al. 2015
<i>L. unicellulare</i>	MD6004	KX505376	Crous & al. 2018
<i>L. voraginesporum</i>	H-22560	KX499520	Crous & al. 2018
<i>Lindgomyces ingoldianus</i>	ATCC 200398	AB521736	Hirayama & al. 2010
<i>L. rotundatus</i>	MAFF 239473	KF314114	Tsang & al. 2014
<i>Magnicamarosporium iriomotense</i>	KT 2822	AB807509	Tanaka & al. 2015
<i>Monocillium mucidum</i>	CBS 980.70	MG826851	Crous & al. 2018
<i>Noosia banksiae</i>	CPC:17282	JF951167	Crous & al. 2011
<i>Periconia cookei</i>	MFLUCC 17-1399	MG333493	Hyde & al. 2018
<i>P. cyperacearum</i>	CPC 32138	MH327851	Crous & al. 2018
<i>P. digitata</i>	CBS 510.77	AB807561	Tanaka & al. 2015
<i>P. homothallica</i>	KT 916	AB807565	Tanaka & al. 2015
<i>P. igniaria</i>	CBS 845.96	AB807567	Tanaka & al. 2015
<i>P. macrospinoso</i>	CBS 135663	KP184038	Knapp & al. 2015
<i>P. pseudodigitata</i>	KT 1395	AB807564	Tanaka & al. 2015
<i>P. thailandica</i>	MFLUCC 17-0065	KY753888	Liu & al. 2017
<i>Pleurophoma acaciae</i>	CPC 29188	KY173524	Crous & al. 2013
<i>Preussia fleischhakii</i>	CBS 565.63	GQ203721	Kruys & Wedin 2009
<i>P. terricola</i>	CBS 527.84	GQ203724	Kruys & Wedin 2009
<i>P. typharum</i>	CBS 107.69	GQ203726	Kruys & Wedin 2009
<i>Pseudodictyosporium thailandica</i>	MFLUCC 16-0029	KX259522	Wang & al. 2016
<i>Spadicoides bina</i>	CBS 137794	KY931824	Réblová & al. 2018
<i>S. fuscolutea</i>	CBS 141263	KY931826	Réblová & al. 2018
<i>S. hyalostoma</i>	CBS 139771	KY931830	Réblová & al. 2018
<i>Sporidesmium tengii</i>	HKUCC 10837	DQ408559	Shenoy & al. 2006
<i>Sporormia fimetaria</i>	UPS: Lundqvist 2302-c	GQ203728	Kruys & Wedin 2009
<i>Sporormiella megalospora</i>	UPS:Kruys 305	GQ203743	Kruys & Wedin 2009

DNA extraction, amplification, alignment, and phylogenetic analysis

The INIFAT-2483 and INIFAT-2457 isolates were cultured on V8 for 10 days at 25°C under near UV in a 12 h dark/light cycle. DNA extraction followed a modified protocol from Ceniz (1992). The primer pair LROR/LR5 was used to amplify the D1/D3 domain of the LSU nrDNA (White & al. 1990). PCR products were purified and sequenced at Macrogen Inc., South Korea. Consensus sequences assembled and edited using Geneious (ver. 10.1.2) were compared with those of the National Center for Biotechnology Information (NCBI) using BLAST.

Alignments for each data set were made in MEGA 6.0 (Tamura & al. 2013) using the ClustalW algorithm (Thompson & al. 1994) and refined with MUSCLE (Edgar 2004). The alignment included our strain sequences and others representing different genera in *Pleosporales* available from NCBI (TABLE 1). A LSU sequence phylogeny was generated using Maximum Likelihood (ML) with the best nucleotide substitution model found in MEGA 6.0 (Tamura & al. 2013). The best model used was Tamura-Nei with Gamma distribution. Bootstrap analysis of 1000 replicates assessed the reliability of the reconstructed phylogenies. ML bootstrap values $\geq 70\%$ were considered significant.

Results

The BLAST query revealed that LSU sequences of *E. parvum* INIFAT-2483 and INIFAT-2457 showed a 99.3% similarity with *E. parvum* [$\equiv$ *Helminthosporium parvum*, ex-type] CBS 190.95 and 92.1% with *Helminthosporium asterinum* Cooke CBS 203.35. However, they showed sequence identity of $<86\%$ with LSU sequences of other *Helminthosporium* species.

We carried out a phylogenetic analysis of the LSU locus to assess the relationships of *Ellismarsporium* with members of the *Pleosporales*. The final analysis encompassed 62 sequences and comprised 552 bp. The ML tree nested all *E. parvum* isolates (INIFAT-2483, INIFAT-2457, CBS 190.95) in a well-supported subclade (bootstrap value = 99%), with *H. asterinum* CBS 203.35 and *Kirschsteiniotelia aethiops* (Sacc.) D. Hawksw. as the closest sister taxa (FIG. 1).

Both morphological and phylogenetic analyses of *E. parvum* support *Ellismarsporium* within *Pleosporales*.

Taxonomy

Ellismarsporium parvum R.F. Castañeda & W.B. Kendr.,

Mycotaxon 132(4): 763 (2017)

FIGS 2, 3

$\equiv$ *Helminthosporium parvum* R.F. Castañeda & W.B. Kendr., Univ.

Waterloo Biol. Ser. 35: 57 (1991), nom. illeg., non Grove (1886)

COLONIES on V8 agar at 25°C attaining 24 mm diam after 10 days, felted, sparsely minutely lanate, greenish olivaceous. CONIDIOPHORES

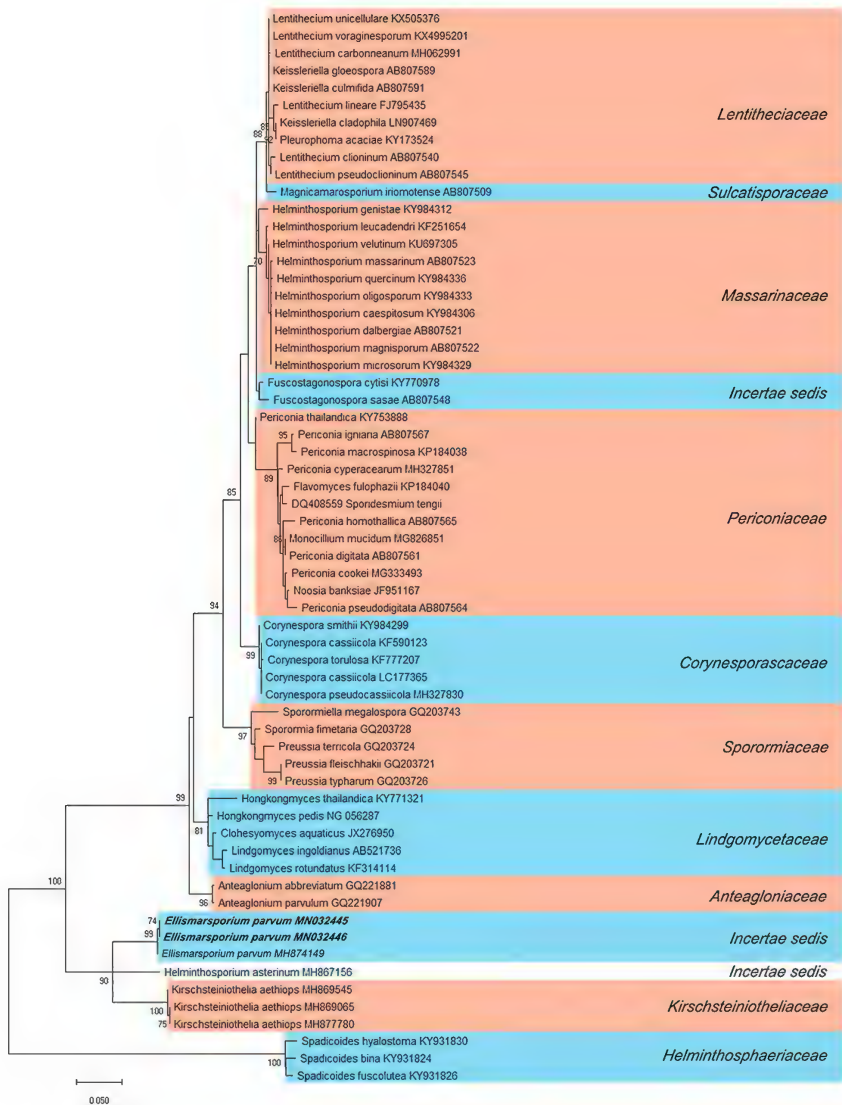


FIG. 1. Maximum Likelihood (ML) tree inferred from LSU sequences of *Ellismarsporium parvum* and related genera, based on 62 sequences. The bootstrap test was conducted with 1000 replicates; bootstrap values $\geq 70\%$ are indicated at the nodes. The scale bar indicates the number of expected changes per site.

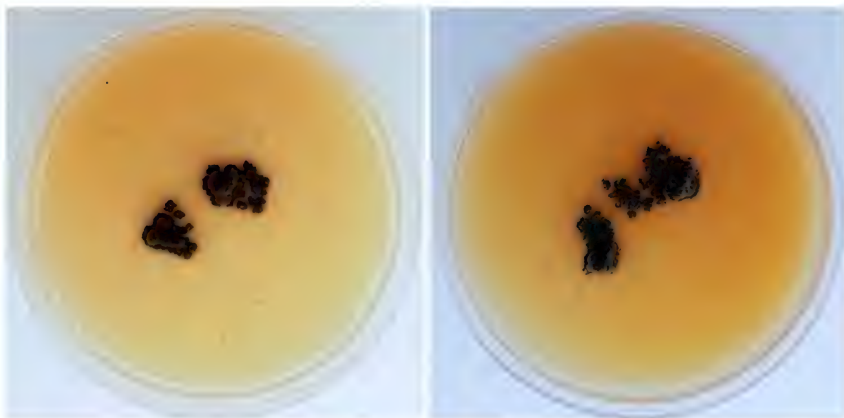


FIG. 2. *Ellismarsporium parvum* (holotype, INIFAT C90/101). Colonies on V8 agar.

macronematous, mononematous, erect, straight or flexuous, unbranched, cylindrical, sometimes slightly clavate or inflated toward the apex, 4–10-septate, brown, smooth, ≤ 220 μm long. CONIDIOGENOUS CELLS polytretic, intercalary and terminal, integrated, cylindrical (terminal cells somewhat clavate to inflated or slightly curved), brown, $10\text{--}40 \times 3\text{--}8$ μm . CONIDIA acropleurogenous, cylindrical-ellipsoidal, cylindrical to oblong (rarely obovoid), 1–2-distoseptate, smooth, brown to smoke-olivaceous-brown, $14\text{--}23 \times 6\text{--}10$ μm , in short branched acropetal chains.

SPECIMENS EXAMINED: CUBA, PINAR DEL RIO PROVINCE, San Juan y Martínez, San Simón de las Cuchillas, $22^{\circ}16'N$ $83^{\circ}50'W$, on bark of *Quercus oleoides* var. *sagrana* (Nutt.) C.H. Mull. [= *Q. cubana* A. Rich.], 24 March 1990, R.F. Castañeda Ruiz (holotype, INIFAT C90/101; INIFAT-2457, GenBank MN032445 [URM 94323 & CCMCIBE-H500]; INIFAT-2483, GenBank MN032446 [URM 94322 & CCMCIBE-H501]).

Helminthosporium varium, published by Alves-Barbosa & al. (2017), is distinguished by distoseptate, long obclavate, subcylindrical, oblong, or navicular, 1–4-septate, irregularly verrucose or verruculose, gray brown to brown conidia produced in branched and unbranched acropetal chains. As the species clearly falls within the *Ellismarsporium* generic concept, we propose a new combination:

Ellismarsporium varium (Alves-Barb., Malosso & R.F. Castañeda) K. Zhang,
Alves-Barb., Malosso & R.F. Castañeda, **comb. nov.**

MB 832010

$\equiv$ *Helminthosporium varium* Alves-Barb., Malosso & R.F. Castañeda,
Nova Hedwigia 105: 67 (2017)

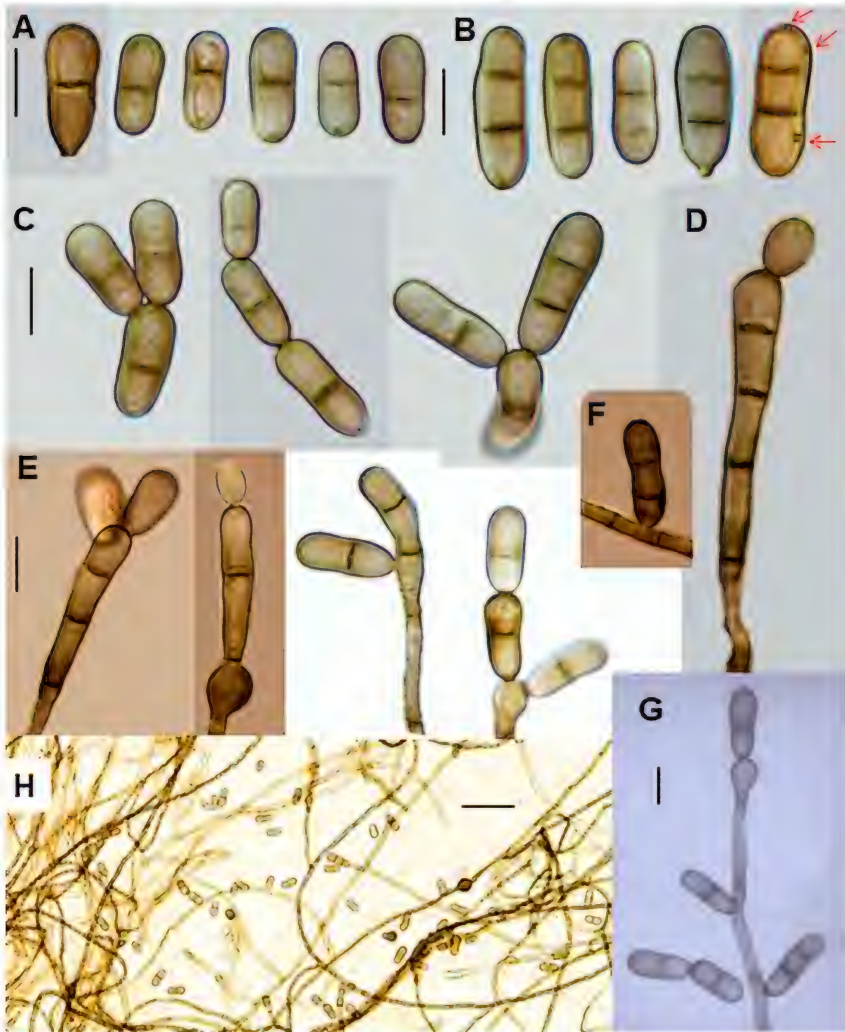


FIG. 3. *Ellismarsporium parvum* (from culture ex holotype INIFAT C90/101). A–C. Conidia; D–G. Conidiogenous cells and conidia; H. Hyphae, conidiophores, conidiogenous cells, and conidia. Scale bars: A–G = 10 µm; H = 50 µm.

Discussion

The phylogenetic placement of *Ellismarsporium* was previously unknown, despite several studies on the phylogenetic relationships of *Pleosporales*

(Hashimoto & al. 2017, Li & al. 2017). Our phylogenetic analysis places *Ellismarsporium* in *Pleosporales*. However, its placement at the family level remains unresolved. Our results show *Ellismarsporium* as sister to the clades of *K. aethiops* (*Kirschsteinioteliaceae*) and *H. asterinum* CBS 203.35 (FIG. 1). As *Ellismarsporium* was proposed in 2017, it is understandable that the genus was not included in recent phylogenetic studies on *Kirschsteinioteliaceae* (Su & al. 2016, Mehrabi & al. 2017, Bao & al. 2018). To determine the placement of *Ellismarsporium* at family level, a study using multiple loci is necessary in the future. Additionally, our results place *H. asterinum* CBS 203.35 distant from the *Helminthosporium* clade (FIG. 1), indicating that species also requires further study.

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***Acarospora scottii* and *Sarcogyne paradoxa* spp. nov. from North America**

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ABSTRACT—*Acarospora scottii*, a facultative lichenicolous lichen on crustose lichens, is described and typified from Minnesota. *Sarcogyne paradoxa*, which is described and typified from California, grows as an endolithic lichen or as a lichenicolous fungus endokaplyic in crustose lichens.

KEY WORDS—*Acarospora americana*, *Acarosporaceae*, New Mexico, *Polysporina*, taxonomy

Introduction

Lichenicolous lichens begin their life cycle as non-lichenized parasites in the microbiomes of lichens, expropriate the algae of the host, and eventually morph out of the host thallus, destroying the host (Diederich & al. 2018; Knudsen & Kocourková 2018a; Knudsen & al. 2012, 2014). They persist as lichenized fungi in a new epilithic thallus that differs from the host form. Two hundred fifty-eight obligatory and facultative species have been reported worldwide (Diederich & al. 2018, Knudsen & Kocourková 2018a). Reports in older literature are not based on this distinction and may not be parasites but crustose lichens that overgrow and destroy other lichens in the competition for space (although winning the competition may bestow a saprobic benefit).

Obligatory lichenicolous lichens always begin their life cycle as juvenile non-lichenized parasites. Obligatory lichenicolous lichens can be host specific. For instance, *Heteropladidium transmutans* K. Knudsen & al. from

the Sonoran Desert has only been found growing out of *Acarospora socialis* H. Magn. and has only been found as an independent lichen in association with populations of its host (Knudsen & al. 2014). Or obligate lichenicolous lichens can be opportunistic, occurring on different species or genera. For instance, *Diploschistes muscorum* (Scop.) R. Sant. parasitizes many different *Cladonia* species and (rarely) is parasitic on *Lepraria xerophila* Tønsberg and *Leprocaulon americana* Lendemer & B.P. Hodk. in coastal habitats in southern California (Kocourková & al. 2012).

Facultative lichenicolous lichens can begin as a non-lichenized parasite in the microbiome of a lichen, although they usually begin their life cycle as non-parasitic lichenized fungi. They are also usually opportunistic, although records may be based on only one host. A classic example of a facultative lichenicolous lichen is *Acarospora succedens* H. Magn. It was described from a single specimen as a parasite on *Dimelaena suboreina* (B. de Lesd.) Hale & W.L. Culb. in New Mexico (Magnusson 1930). The taxon was described again from New Mexico as the non-parasitic lichen *A. interspersa* H. Magn., which is frequent in the Chihuahuan and Sonoran Deserts and is rarely found as a parasite on crustose lichens (Knudsen 2007, 2011; Magnusson 1933). In this paper we describe a facultative lichenicolous lichen, *Acarospora scottii*, from Minnesota and Ontario, Canada.

In contrast to lichenicolous lichens, we describe *Sarcogyne paradoxa* which occurs as either a non-lichenized parasite dwelling in the microbiome of crustose lichens or as an endolithic lichen. It grows in the Mojave Desert and other xerothermic habitats in Asia and North America. The implications of *S. paradoxa* for a revision of species of the polyphyletic genus *Polysporina* is discussed.

Material & methods

A specimen collected by Perry Scott, a citizen lichenologist, and specimens from ASU & UCR herbaria were studied using standard microscopy and spot tests. The amyloid reaction of the hymenial gel and subhymenium was tested with fresh undiluted IKI (Merck's Lugol; see protocol in Knudsen & Kocourková 2018b). Measurements were made in water. Macrophotographs were taken with the Olympus DP74 digital camera mounted on Olympus SZX 16 stereomicroscope equipped with PRO-SZM1 - Focus Drive Motorization for stacking pictures and stacked using Olympus DeepFocus 3.4 module of Promicra QuickPhoto Camera 3.2 software. The figure plates were processed with the same software fitted with Promicra Figure Maker modul and eventually refined with Adobe Photoshop CS4 Extended ver. 11.0.

Taxonomy

Acarospora scottii K. Knudsen & Kocourk., sp. nov.

Figs 1, 2

MB 831962

Similar to *Acarospora americana* but differing in having dark blue hymenial gel in Lugol's (euamyloid), in having a continuous polysaccharide epicortex giving the areoles a dark shiny appearance, and in having a cortex of vertical hyphae.

TYPE: USA, Minnesota, Cook. Co., Superior National Forest, Caribou Rock Trail, on vertical east-facing side of Caribou Rock, 48.06380°N 90.45655°W, 560 m, on unknown crustose lichen and *Aspicilia* species and independent on diabase, 6 August 2017, P.A. Scott 5416 (Holotype, PRM!)

ETYMOLOGY: Named in honour of the collector, citizen lichenologist Perry Scott, who collected the new species.

HYPOTHALLUS endolithic, continuous with medulla, no algae observed, broadly and firmly attached or becoming loosely attached and squamulose, replicating by division. THALLUS of areoles ≤ 1.3 mm wide, round to angular, flat to bullate, 300–500 μm thick, broadly attached, replicating by division. Upper surface dark brown, shiny, epruinose, black edged. Lower surface usually dark brown. Epicortex 5 μm thick, continuous. Cortex 30–50 μm thick, of distinct vertical hyphae, 2–3 μm wide, breaking up into irregular cells, terminating in expanded apices, 4–5 μm wide in dark brown gel cap, upper layer of cortex dark brown, c. 10 μm high, lower layer hyaline. Algal layer continuous without hyphal bundles, 50–100 μm thick, algal cells 10–15 μm wide. Medulla 150–300 μm thick, hyphae thin-walled, 2–3 μm diam.

APOTHECIA usually 1 per areole, rarely 2 to 6, immersed ≤ 1 mm wide, the disc epruinose, rugulose, usually round. Parathecium indistinct or narrow to 15 μm wide, intergrading with cortex. Epihymenium 10–20 μm thick, coherent, brown to yellowish brown, sealed with polysaccharide hyaline layer c. 5 μm , a continuation of the epicortex. Hymenium (including epihymenium) 100–120(–150) μm tall, highest in bullate areole, hymenial gel IKI+ blue (euamyloid). Paraphyses 1.5–2 μm diam. at mid-level, apices expanded to 3 μm in pigment cap with blackish pigment mark, often with abundant oil drops. Asci 70–90 $\times$ (8–)10–12(–15) μm , narrow, c. 100 ascospores per ascus. Ascospores 3–4(–5) $\times$ 1.5–2 μm . Subhymenium 30–50 μm thick, IKI+ blue (euamyloid). Hypothecium 10 μm wide. PYCNIDIA not observed. Spot tests negative, K–, KC–, C–, P–.

SELECTED ADDITIONAL SPECIMENS EXAMINED: CANADA. ONTARIO. Thunder Bay District, Sleeping Giant Provincial Park, by shore of Lake Superior, 48.31463°N 88.88739°W, 190 m, on diabase bedrock and on *Aspicilia* species, 7 September 2019,

P.A. Scott 7030 & J. Hollinger (hb. Scott). USA. MINNESOTA, Cook Co., Boundary Waters Canoe Area Wilderness, near west end of Mountain Lake, 48.09710°N, 90.28500°W, 595 m, on *Aspicilia* species on northwest facing diabase rocks near top of cliff, 15 August, 2019, P.A. Scott 6837 (hb. Scott), Superior National Forest, southwest-facing cliff overlooking Moss Lake, 48.0654°N 90.4611°W, on diabase, 5 August 2017, P.A. Scott 5405A (hb. Scott), Caribou Rock, Caribou Rock Trail, on exposed vertical east-facing rock near top of cliff, 48.06380°N, 90.45640°W, 560 m, on *Aspicilia* species and on diabase, 11 August 2019, P.A. Scott 6767 (NY), 6768 (hb. Scott).

ECOLOGY & DISTRIBUTION. Epilithic on diabase and/or parasitic on crustose lichens in North America. Diabase sills form the caps of the cliffs in this area of Minnesota. Expected to be more widespread in United States and Canada on other intermediate siliceous rocks poor in SiO₂, possibly also on more acid rock. Specimens in herbaria are probably identified as *A. americana* H. Magn. or *A. veronensis* A. Massal.

DISCUSSION. *Acarospora scottii* is similar to *A. americana* but differs in having areoles that are not dull brown but shiny due to a continuous polysaccharide epicortex and in having a consistent black margin around the edge of areole and becoming squamulose with dark brown to black lower surface. It also differs in having euamyloid hymenial gel in Lugol's vs. hemiamyloid hymenial gel in Lugol's and in having a cortex of vertical or irregular hyphae vs. distinctly paraplectenchymatous hyphae (Knudsen & al. 2011). *Acarospora americana* has a parathecium that usually widens around the apothecial disc, even forming an elevated parathecial crown the same color as thallus. *Acarospora scottii* has an indistinct or narrow parathecium, often intergrading with the cortex, but in some specimens may have a raised thalline collar surrounding and higher than the apothecial disc.

Acarospora veronensis differs from *A. scottii* in having a narrow cortex (c. 15 µm vs. 30–50 µm thick) and in having hemiamyloid hymenial gel in Lugol's.

Acarospora scottii is a typical facultative lichenicolous lichen. Its non-lichenized hypothallus spreads through the upper layer of the rock. In patches of bare rock, the hypothallus parasitizes algae forming an epilithic lichen thallus. Spreading under crustose lichens, the hypothallus penetrates them from below, expropriating the algal photobiont from the host, eventually destroying the mycobiont. It morphs out of the host forming an epilithic lichen thallus. In *A. scottii*, the areoles that emerged from crustose lichens are much more robust, thicker or bullate than the areoles growing on bare rock (Figs 1, 2). This suggests that not only are they receiving nutrition from the photobiont of the host but also from the saprobic absorption of the



FIG. 1. *Acarospora scottii* (holotype, PRM – Scott 5416). A. Areoles emerging from unknown crustose lichen; B. Thick or bullate areoles emerging from *Aspicilia* thallus. Scale bars = 1 mm.

mycobiont of the host. Such a difference is not distinctive in other facultative lichenicolous lichens we have studied, for instance *A. schleicheri* (Ach.) A. Massal. Like most facultative lichenicolous lichens it is opportunistic and

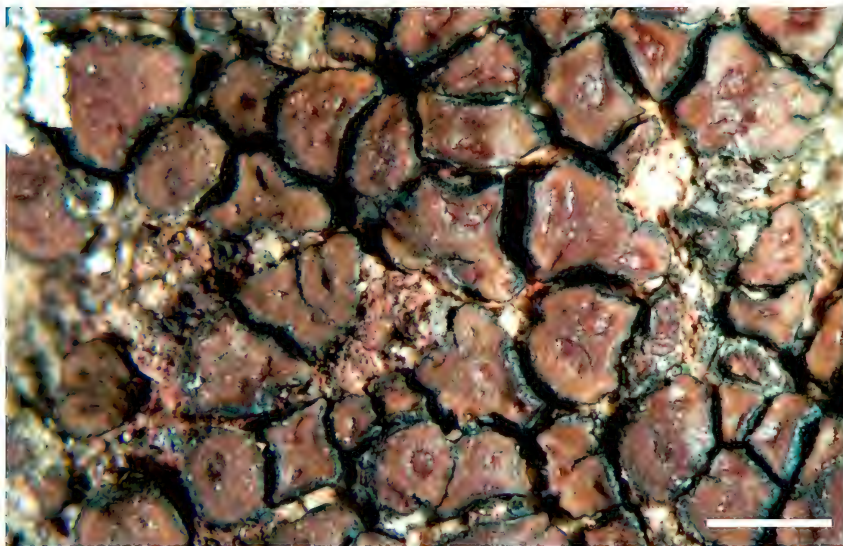


FIG. 2 *Acarospora scottii* (holotype, PRM – Scott 5416).
Areolate thallus with flat areoles growing on bare rock. Scale bar = 1 mm.

not host specific (in holotype it occurs on *Aspicilia* species and unknown crustose lichen). The paratype was non-lichenicolous.

Areoles in the holotype were often sterile or with only a few mature asci. The holotype was collected during summer in Minnesota, suggesting ascospores are released seasonally, possibly early spring, at least in Minnesota.

***Sarcogyne paradoxa* Kocourk. & K. Knudsen, sp. nov.**

FIG. 3

MB 831963

Differs from *Acarospora subfuscens* by its reddish brown to brown apothecia that remain brown when hydrated.

TYPE: USA, California, San Bernardino Co., Joshua Tree National Park, below Belle Mountain, in unnamed wash, 34.0189°N 116.0025°W, 1382 m, common on granite boulder on wash, apothecia emerging from rock, 22 August 2005, K. Knudsen 3620 (Holotype, UCR; isotype, ASU).

ETYMOLOGY: Named because it grows as either an endolithic lichen or a lichenicolous fungus.

THALLUS in non-parasitic specimens endolithic, the algal layer occurring in the substrate below the apothecia beneath a mycelial base continuous with hypothecium. In parasitic specimens endokapylic, no algal layer occurring in substrate below host, apothecia emerging from the host.

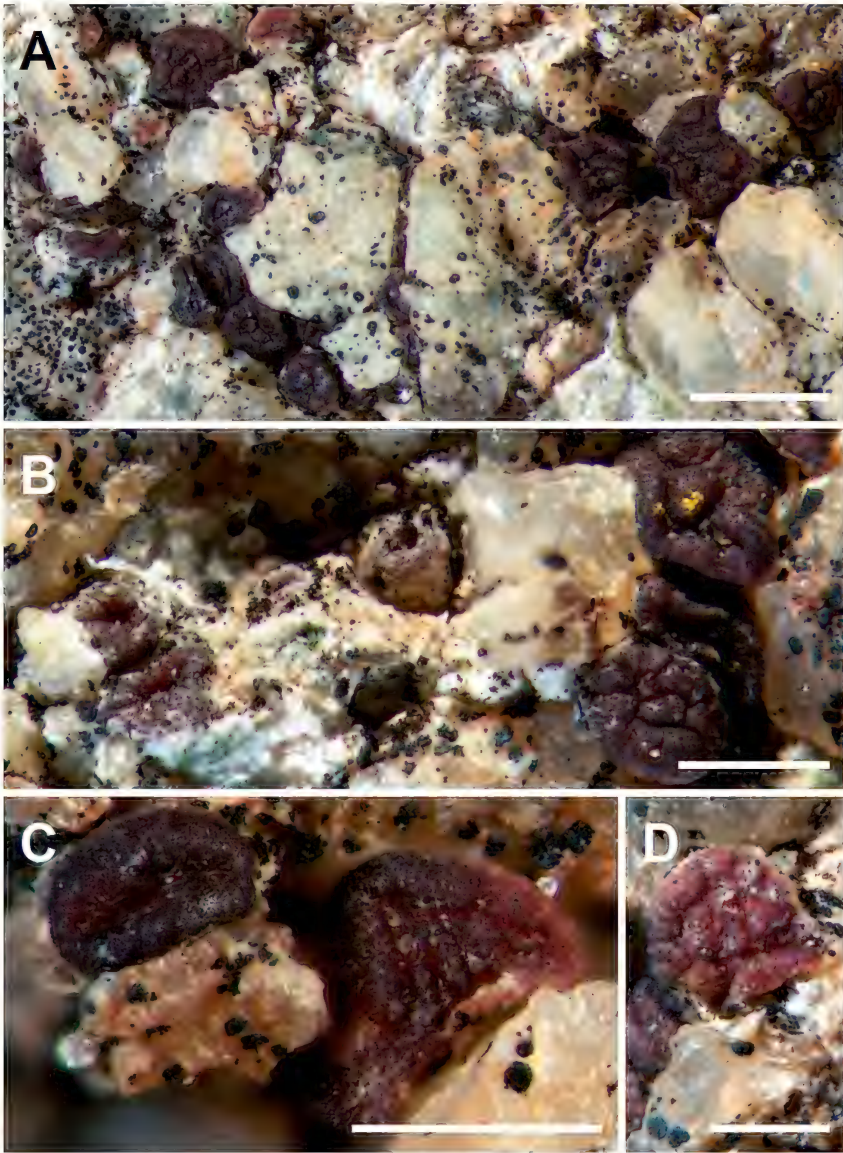


FIG. 3 *Sarcogyne paradoxa* (holotype, UCR – Knudsen 3620). A. Habit of the thallus in rock crevices (with *Lichenothelia* species); B. Emerging and developed apothecia; C. Apothecia with conspicuous elevated margins; D. Fully developed apothecium with rugose surface. Scale bars: A = 1 mm; B, C = 500 μ m; D = 200 μ m.

APOTHECIA superficial on host or occurring on substrate, brown when dry or wet, 0.5–1.0 mm diam, round or irregular, dispersed or contiguous, forming clusters of apothecia to 3 mm wide; disc brown to reddish brown, convex, with furrows, ridges, and umbos, rough and uneven, margin distinct but becoming fissured. Parathecium to 100 μ m wide, hyphae mostly 2–3 μ m diam, septate, cells mostly 2–3 μ m wide, ending in expanded apices forming outer wall of the margin. Outer layer of margin reddish-brown to dull brown, 20–30 μ m thick; inner layer hyaline. Epihymenium 10–20 μ m thick, in reddish brown gel, accretions on surface of disc to 200 μ m high formed from the epihymenial gel. Hymenium 80–120 μ m tall, hyaline, hymenial gel IKI+ deep blue (euamyloid), paraphyses coherent (1–)2–3 μ m diam, sometimes constricted at septa, infrequently branching in lower half, unexpanded or expanded apices sometimes in darker pigment caps. Asci 60–90 $\times$ 12–20 μ m, ascospores mostly 100 per ascus, ascospores (3.0–)4.0–4.5(–7) $\times$ 2.0–3.0 μ m, mostly broadly ellipsoid. Subhymenium hyaline, 30–50 μ m thick, IKI+ blue. Hypothecium up to 50 μ m thick, continuous with vegetative vertical hyphae forming a mycelial base above algal layer in substrate. **PYCNIDIA** not seen. Spot tests C–, KC–, K–. P–.

SELECTED ADDITIONAL SPECIMENS EXAMINED: **CALIFORNIA**, **San Bernardino Co.**, Granite Mountains: Sweeney Granite Mountains UC Reserve, Sibyl Allison trail, 34.7892°N 115.6717°W, 1692 m, on granite, 14 December 2007, K. Knudsen 8050 & R. Muerter (UCR). **Santa Barbara Co.**, Channel Island National Park, Santa Rosa Island, south slope of South Peak, 33.9064°N 120.1283°W, 243 m, on unknown host and independent on sandstone, 15 August 2007, K. Knudsen 8762.2 (UCR). **San Luis Obispo Co.**, San Simeon, San Simeon State Park, Molinari Property, exposed slab of volcanic rock next to ravine along old Highway One dirt road, 35.6039°N 121.1275°W, 41 m, on crustose lichen, 8 January 2007, K. Knudsen 8116 (UCR)

ECOLOGY & DISTRIBUTION. Occurring in siliceous rock, usually granite, as an endolithic lichen or endokapylic in the thallus of crustose lichens as a non-lichenized parasite in North America (California) and Asia (Afghanistan, Xinjiang in China) (Knudsen & Kocourková 2008, 2009; L. Nurtai, pers comm.) The specimen from Afghanistan at GZU is a parasite on an unknown lichen on granite. The specimens from Xinjiang are endolithic lichens on granite. Based on the distribution of *Acarospora gyrocarpa* (H. Magn.) K. Knudsen & M. Westb. [$\equiv$ *Polysporina gyrocarpa* (H. Magn.) N.S. Golubk.] in China and southwestern United States, *S. paradoxa* is expected like *A. gyrocarpa* to be widespread but probably rare in the Chihuahuan, Mojave, and Sonoran Deserts in southwestern North America. (Knudsen & Kocourková 2009). The species is easily over-looked in field inventories.

DISCUSSION. *Sarcogyne paradoxa* differs from the lichenicolous fungus *Acarospora subfuscescens* (Nyl.) H. Magn. in having brown apothecia with epihymenial accretions that are brown when hydrated instead of dark brownish black to black apothecia with epihymenial accretions that are black when hydrated (Knudsen & Kocourková 2008). *Sarcogyne paradoxa* was treated previously as *Polysporina arenacea* (H. Magn.) K. Knudsen & Kocourk. [a misapplication] and was only subsequently recognized as a lichenicolous fungus (Knudsen & Kocourková 2008). *Acarospora arenacea* H. Magn. is a rare lichen known only from Utah and North Dakota, USA (Magnusson 1952). In phylogenetic analyses *S. paradoxa* falls into the *Sarcogyne* lineage (Westberg & al. 2015, Knudsen & al. 2019).

Sarcogyne paradoxa has a different lifestyle from lichenicolous lichens like the obligatory *Diploschistes muscorum* or the facultative *Acarospora scottii*. It can be a lichen; the hyphae of the hypothallus parasitizes algae occurring in rock in the upper 1 mm of the substrate, forming an endolithic lichenized thallus that eventually produces epilithic apothecia. Or it can be a lichenicolous fungus, the endolithic hypothallus apparently entering the host from beneath the thallus. It does not expropriate the algae of the host like a lichenicolous lichen, eventually forming an independent epilithic thallus. Like many lichenicolous fungi, it expropriates a portion of the carbon produced by the photobiont of the lichen host but maintains a symbiotic relationship, not destroying the host. In the few specimens seen, it does appear to suppress the host forming apothecia, which would conserve for its nutrition carbon produced by the photobiont of the host that would otherwise nourish the sexual reproduction of the host.

During our work on the genus *Polysporina* Vězda, we used broad morphological and anatomical species concept of *Polysporina subfuscescens* (Nyl.) Knudsen & Kocourk. for identifying taxa growing on lichens and a broad concept of *Polysporina simplex* (Borrer ex Hooker) Vězda for identifying lichenized taxa growing on rock (Knudsen & Kocourková 2008; Westberg & al. 2015). Based on phylogenetic analyses of a large sampling of specimens, *Polysporina* was found to be polyphyletic with most taxa occurring in several different lineages of *Acarospora* (Westberg & al. 2015). In that tree, the lineages *Polysporina* A and *Polysporina* B contained specimens identified as *P. subfuscescens* (lichenicolous fungus) and *P. simplex* (endolithic lichen). These two lineages apparently represent single species, both of which either occur as a lichenicolous fungus or an endolithic lichen like *Sarcogyne paradoxa*. Because *Polysporina* is polyphyletic and negated as

a monophyletic genus, we treat the taxa as *Acarospora* or *Sarcogyne* based on their position in the current phylogenetic trees of *Acarosporales* (Westberg & al. 2015; Knudsen & al. 2019). *Acarospora subfuscescens* and *Acarospora simplex* (Borrer ex Hooker) Jatta are heterogeneous in these phylogenetic analyses and obviously in need of a revision (Gueidan & al. 2014, Westberg & al. 2015).

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Regional annotated mycobiota new to the Mycotaxon website

ABSTRACT—We are pleased to announce that we uploaded our 138th free access funga to the MYCOTAXON mycobiota site in May. Everyone is invited to download the 14-page “A checklist of marine fungi from Australia” by Fryar, Hyde, and Catcheside via: <http://www.mycotaxon.com/mycobiota/index.html>

AUSTRALASIA

Australia

SALLY C. FRYAR, KEVIN D. HYDE, DAVID E.A. CATCHESIDE. A checklist of marine fungi from Australia. 14 p.

ABSTRACT—A checklist of non-lichenized marine fungi in Australia is presented. From 1954 to 2020 a total of 121 species in 93 genera were observed. Most species were ascomycetes, with only three basidiomycetes. Of these ascomycetes, most were seen in their sexual state (93 species) compared with their asexual state (21 species).

KEY WORDS—biodiversity, fungal diversity

Regional annotated mycobiota new to the Mycotaxon website

ABSTRACT—MYCOTAXON announces the posting of its 139th free access funga to its mycobiota site in June. The 42-page checklist of Brazilian corticioid fungi by Chikowski, Lira, Larsson, and Gibertoni may be downloaded from our website via <http://www.mycotaxon.com/mycobiota/index.html>

SOUTH AMERICA

Brazil

RENATA S. CHIKOWSKI, CARLA R.S. DE LIRA, KARL HENRIK LARSSON, TATIANA B. GIBERTONI. A checklist of corticioid fungi (*Agaricomycetes*, *Basidiomycota*) from Brazil. 42 p.

ABSTRACT—This study updates the available data about species of corticioid fungi from Brazil. We based our compilation on literature, herbarium revisions, and added information from recent field trips in the Atlantic Rain Forest, Amazonia, Caatinga, and Cerrado phytogeographic domains. Currently, there are 367 accepted species of corticioid fungi recorded in Brazil. Those representing new records include four for the Neotropics, 15 for the country, 18 for Northeast Brazil, and 41 for Brazilian phytogeographic domains.

KEY WORDS—diversity, *Hymenochaetales*, *Polyporales*, resupinate fungi, *Russulales*

Regional annotated mycobiota new to the Mycotaxon website

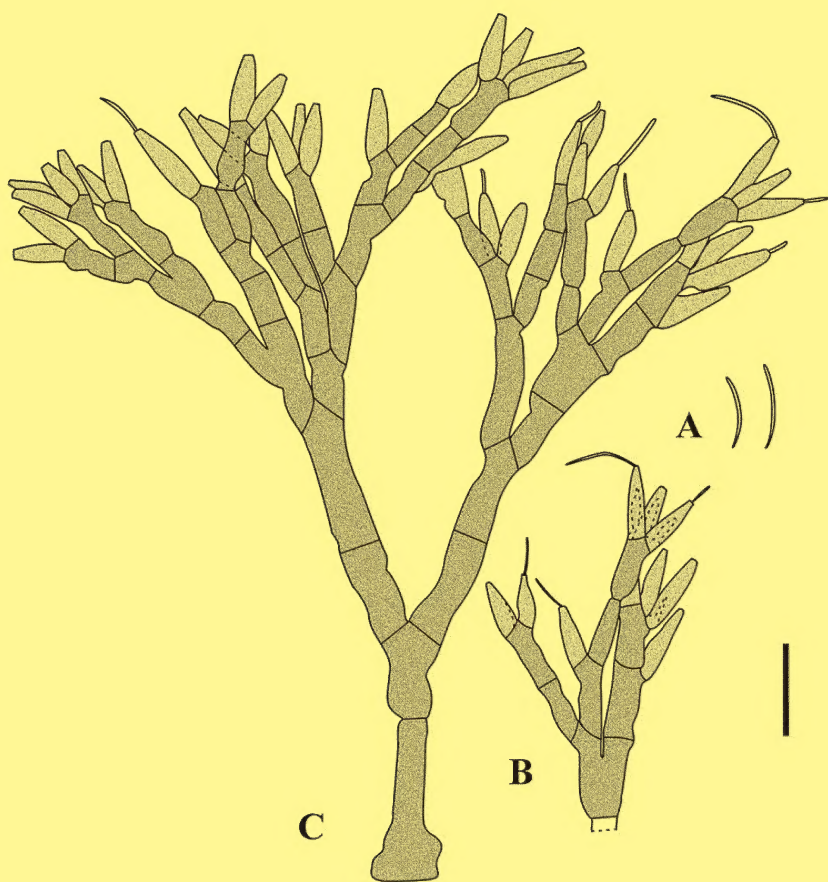
ABSTRACT—MYCOTAXON announces the posting of its 140th free access funga to its mycobiota site in June. This excellent 18-page global checklist of aquatic arbuscular mycorrhizal fungi by Queiroz, Jobim, Vista, Leroy, Gomes, and Goto may be downloaded from our website via <http://www.mycotaxon.com/mycobiota/index.html>

GLOBAL

MARIANA BESSA DE QUEIROZ, KHADIJA JOBIM, XOCHITL MARGARITO VISTA, JULIANA APARECIDA SOUZA LEROY, STEPHANIA RUTH BASÍLIO SILVA GOMES, BRUNO TOMIO GOTO. Occurrence of *Glomeromycota* species in aquatic habitats: a global overview. 18 p.

ABSTRACT—Arbuscular mycorrhizal fungi (AMF) are recognized in terrestrial and aquatic ecosystems. The latter, however, have received little attention from the scientific community and, consequently, are poorly known in terms of occurrence and distribution of this group of fungi. This paper provides a global list on AMF species inhabiting aquatic ecosystems reported so far by scientific community (lotic and lentic freshwater, mangroves, and wetlands). A total of 82 species belonging to 5 orders, 11 families, and 22 genera were reported in 8 countries. Lentic ecosystems have greater species richness. Most studies of the occurrence of AMF in aquatic ecosystems were conducted in the United States and India, which constitute 45% and 78% reports coming from temperate and tropical regions, respectively.

KEY WORDS—checklist, flooded areas, mycorrhiza, taxonomy



Ramiphialis ronuroensis sp. nov.

(Barbosa & al.— FIG. 2, p. 296)

PATRICIA OLIVEIRA FIUZA, artist